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OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:10:12 : Search time 48 Seconds
(without alignments)
121.393 Million cell updates/sec

Title: US-09-606-804-1
Perfect score: 19
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
- 2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
- 3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/prodata/1/lna/PCUTS.COMB.seq:*
- 6: /cgn2_6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	10	52.6	272 1	US-08-248-474-36 Sequence 36, Appl
2	10	52.6	272 3	US-08-756-849-36 Sequence 36, Appl
3	10	52.6	296 2	US-08-716-942-20 Sequence 20, Appl
4	10	52.6	296 4	US-09-130-337A-20 Sequence 20, Appl
5	10	52.6	360 6	5196523-1 Patent No. 5196523
6	10	52.6	387 4	US-08-804-372A-23 Sequence 23, Appl
7	10	52.6	392 4	US-09-404-879A-372 Sequence 372, Appl
8	10	52.6	399 6	5196523-23 Patent No. 5196523
9	10	52.6	421 6	5196523-22 Patent No. 5196523
10	10	52.6	424 1	US-08-609-657-15 Sequence 15, Appl
11	10	52.6	467 4	US-09-257-584-8 Sequence 8, Appl
12	10	52.6	531 4	US-09-222-575-123 Sequence 123, Appl
13	10	52.6	754 4	US-09-020-956-20 Sequence 20, Appl
14	10	52.6	754 4	US-09-030-607-20 Sequence 20, Appl
15	10	52.6	754 4	US-09-605-785-20 Sequence 20, Appl
16	10	52.6	754 4	US-09-439-313-20 Sequence 20, Appl
17	10	52.6	754 4	US-09-352-616A-20 Sequence 20, Appl
18	10	52.6	754 4	US-09-232-149A-20 Sequence 20, Appl
19	10	52.6	843 4	US-09-171-209-38 Sequence 38, Appl
20	10	52.6	849 4	US-08-998-416-552 Sequence 552, Appl
21	10	52.6	904 4	US-09-541-941B-21 Sequence 21, Appl
22	10	52.6	1050 4	US-09-137-855-1 Sequence 1, Appl
23	10	52.6	1117 4	US-09-347-819-5 Sequence 5, Appl
24	10	52.6	1137 4	US-09-134-001C-1855 Sequence 1855, Appl
25	10	52.6	1137 4	US-09-541-941B-27 Sequence 27, Appl
26	10	52.6	1347 2	US-08-286-819A-7 Sequence 7, Appl
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28	10	52.6	1347 3	US-08-980-357-7 Sequence 7, Appl
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35	10	52.6	1617 3	US-08-344-639E-25 Sequence 25, Appl
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56	10	52.6	2034 4	US-09-210-993A-1 Sequence 1, Appl
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74	10	52.6	2588 4	US-09-087-465-7 Sequence 7, Appl
75	10	52.6	2606 1	US-08-408-318-1 Sequence 1, Appl
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78	10	52.6	2885 2	US-08-791-849A-15 Sequence 15, Appl
79	10	52.6	3061 1	US-09-570-842-1 Sequence 1, Appl
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81	10	52.6	3280 4	US-09-484-970B-43 Sequence 43, Appl
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83	10	52.6	3292 1	US-08-258-442-12 Sequence 12, Appl
84	10	52.6	3292 5	US-08-328-809-7 Sequence 7, Appl
85	10	52.6	3292 5	PCT-US92-11107-12 Sequence 12, Appl
86	10	52.6	3420 3	US-09-039-859-8 Sequence 8, Appl
87	10	52.6	3720 4	US-09-342-681C-12 Sequence 12, Appl
88	10	52.6	3736 4	US-09-600-776-10 Sequence 10, Appl
89	10	52.6	3981 3	US-09-008-979A-7 Sequence 7, Appl
90	10	52.6	3981 4	US-09-460-618-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-248-474-36
Sequence 36, Application US/08248474
Patent No. 5612471
GENERAL INFORMATION:

APPLICANT: MCK, BIRD, David
APPLICANT: WILSON, Mark A.
TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,474
FILING DATE: 25-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
ORGANISM: Red
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..272
OTHER INFORMATION: /standard_name="DB# 155"
US-08-248-474-36
Query Match 52.6%; Score 10; DB 1; Length 272;
Best Local Similarity 52.6%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 CCAATNNNNNNNNCCAGC 19
DB 97 CCAATATTATTTCACG 115
RESULT 2
US-08-756-849-36
Sequence 36, Application US/08756849
Patent No. 6093810
GENERAL INFORMATION:
APPLICANT: Bird, David MCK.
APPLICANT: Wilson, Mark A.
TITLE OF INVENTION: Nematode-Induced Genes in Tomato
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,849
FILING DATE: 26-NOV-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,474
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-053510US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..272
OTHER INFORMATION: /standard_name="DB# 155"
US-08-756-849-36
Query Match 52.6%; Score 10; DB 3; Length 272;
Best Local Similarity 52.6%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 CCAATNNNNNNNNCCAGC 19
DB 97 CCAATATTATTTCACG 115
RESULT 3
US-08-716-942-20/C
Sequence 20, Application US/08716942
Patent No. 5849491
GENERAL INFORMATION:
APPLICANT: Terragen Diversity Inc.
APPLICANT: Radomski, Christopher C. A.
APPLICANT: Seow, Kah Tong
APPLICANT: Warren, R. Anthony J.
TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,942
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,157
FILING DATE: 20-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson

REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: TERR.P-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 296
TYPE: nucleic acid
STRANDEDNESS: DOUBLE
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM:
FEATURE:
NAME/KEY: fragment of xylanase gene from degenerate primer
US-08-716-942-20
NAME/KEY: amplification of soil DNA

Query Match 52.6%; Score 10; DB 2; Length 296;
Best Local Similarity 52.6%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 217 CCAATGTTGTGCCACG 199

RESULT 4
US-09-130-337A-20/c
Sequence 20, Application US/09130337A
Patent No. 6441148
GENERAL INFORMATION:
APPLICANT: Radomski, CCA
APPLICANT: Seow, KT
APPLICANT: Warren, RAJ
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIO
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 9993-004
CURRENT APPLICATION NUMBER: US/09/130,337A
CURRENT FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 08/716,942
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: 60/004,157
PRIOR FILING DATE: 1995-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 20
LENGTH: 296
TYPE: DNA
ORGANISM: Unknown organism
FEATURE:
OTHER INFORMATION: Description of unknown organism: soil microbe
US-09-130-337A-20

Query Match 52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 217 CCAATGTTGTGCCACG 199

RESULT 5
5196523-1
Patent No. 5196523
APPLICANT: LEE, AMY S.

TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
CALCIUM AND TEMPERATURE
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/354,988
FILING DATE: 19-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 690,951
FILING DATE: 01-JAN-1985
SEQ ID NO: 1
LENGTH: 360
5196523-1

Query Match 52.6%; Score 10; DB 6; Length 360;
Best Local Similarity 52.6%; Pred. No. 3.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 282 CCAATCGAGGCTCCACG 300

RESULT 6
US-08-804-372A-23
Sequence 23, Application US/08804372A
Patent No. 6183753
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,372A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2552/39115E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-804-372A-23

Query Match 52.6%; Score 10; DB 4; Length 387;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 262 CCAATCAAAAGCTGCCACG 280

RESULT 7
US-09-404-879A-372/C
; Sequence 372, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-372

Query Match 52.6%; Score 10; DB 4; Length 392;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 37 CCAATCCAGAGCTCCACG 19

RESULT 8
5196523-23
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO: 23
; LENGTH: 399
5196523-23

Query Match 52.6%; Score 10; DB 6; Length 399;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 311 CCAATCGAGAGCTCCACG 329

RESULT 9
5196523-22
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO: 22
; LENGTH: 421
5196523-22

Query Match 52.6%; Score 10; DB 6; Length 421;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 311 CCAATCGAGAGCTCCACG 329

RESULT 10
US-08-609-657-15
; Sequence 15, Application US/08609657
; Patent No. 5681706
; GENERAL INFORMATION:
; APPLICANT: Anderson, Garth R.
; APPLICANT: Estes, Scott D.
; APPLICANT: Stoler, Daniel L.
; TITLE OF INVENTION: Mammalian Anoxia-Responsive Regulatory
; TITLE OF INVENTION: Element
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Wordperfect for Windows 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,657
; FILING DATE: 01 March 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551,0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-609-657-15

Query Match 52.6%; Score 10; DB 1; Length 424;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 361 CCAATTGATGTACCACG 379

RESULT 11
US-09-257-584-8/C
; Sequence 8, Application US/09257584A

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Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
FILE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 467
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: cab-10 promoter
NAME/KEY: unsure
LOCATION: (370)
OTHER INFORMATION: Nucleotide at this position may be a or g or c or
US-09-257-584-8

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 467;
Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 266 CCAATCACCTCTCCACG 248

RESULT 12
US-09-222-575-123
Sequence 123, Application US/09222575
GENERAL INFORMATION:
APPLICANT: Yuglu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
FILE REFERENCE: 210121.470
CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 123
LENGTH: 531
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: modified_base
LOCATION: (152)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (482)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (373)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (494)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (496)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (502)
OTHER INFORMATION: where n is a, c, g or t
US-09-222-575-123
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 531;
Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    ||||| |||||
Db 506 CCAATTTCAGCACCACG 524

RESULT 13
US-09-020-956-20
Sequence 20, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-020-956-20

Query Match
Best Local Similarity 57.9%; Score 10; DB 4; Length 754;
Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    ||||| | |||||
Db 303 CCAATTGTTTNGCCACG 321

RESULT 14
US-09-030-607-20
Sequence 20, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
```

```
STATE: MA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-20

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 754;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGTTTTCGACG 321

RESULT 15
US-09-605-785-20
Sequence 20, Application US/09605785
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(754)
```

```
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-20

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 754;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGTTTTCGACG 321

RESULT 16
US-09-439-313-20
Sequence 20, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(754)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-20

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 754;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGTTTTCGACG 321

RESULT 17
US-09-352-616A-20
Sequence 20, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
```

```

: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(754)
: OTHER INFORMATION: n = A,T,C or G
US-09-352-615A-20

Query Match
Best Local Similarity 57.9%; Score 10; DB 4; Length 754;
Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATTNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 303 CCAATTGTTTNGCCAGC 321

RESULT 18
US-09-232-149A-20
: Sequence 20, Application US/09232149A
: Patent No. 6465611
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
: FILE REFERENCE: 210121.427C6
: CURRENT APPLICATION NUMBER: US/09/232,149A
: CURRENT FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 338
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 754
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(754)
: OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-20

Query Match
Best Local Similarity 57.9%; Score 10; DB 4; Length 754;
Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATTNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 303 CCAATTGTTTNGCCAGC 321

RESULT 19
US-09-171-209-38
: Sequence 38, Application US/09171209
: Patent No. 6448000
: GENERAL INFORMATION:
: APPLICANT: VANDERBILT UNIVERSITY
: APPLICANT: 305 KIRKLAND HALL
: APPLICANT: NASHVILLE, TN 37240
: TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
: INFECTION
: NUMBER OF SEQUENCES: 83
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Needle & Rosenberg, P.C.
: STREET: 127 Peachtree Street, Suite 1200
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303-1811
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
```

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: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/171,209
: FILING DATE: 08-Mar-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/06067
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Selby, Elizabeth
: REGISTRATION NUMBER: 38,298
: REFERENCE/DOCKET NUMBER: 22000.0061/P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404 688 0770
: TELEFAX: 404 688 9880
: INFORMATION FOR SEQ ID NO: 38:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 843 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-171-209-38

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 843;
Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATTNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 638 CCAATTGTATGTAAACCAGC 656

RESULT 20
US-08-998-416-552
: Sequence 552, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Pohlmann, Peter
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christine
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtle, Philipp
: APPLICANT: Redischung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII
: AND USES THEREOF
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264artis Corporation
: STREET: 3054 Cornwells Road
: CITY: Research Triangle Park
: STATE: No. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
```

```

; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 552:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 849 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1384UP
; US-08-998-416-552

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 849;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 690 CCAATATACCTGCTCCACG 708

RESULT 21
US-09-541-941B-21/C
; Sequence 21, Application US/09541941B
; Patent No. 6309840
; GENERAL INFORMATION:
; APPLICANT: Wang, Jun
; APPLICANT: Shaw, Pang Chui
; APPLICANT: Paul, Pul-Hay
; APPLICANT: Ngan, But-and Fai Ngor Karenda Ngan
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
; FILE REFERENCE: 2913/52188-2A
; CURRENT APPLICATION NUMBER: US/09/541,941B
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 904
; TYPE: DNA
; ORGANISM: Campanumoea Javanica Blume
; US-09-541-941B-21

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 904;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 646 CCAATATCCCTCCACG 628

RESULT 22
US-09-137-855-1/C
; Sequence 1, Application US/09137855B
; Patent No. 6242237
; GENERAL INFORMATION:
; APPLICANT: Kofod, Lene V.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Andersen, Lene N.
; APPLICANT: Clausen, Ib G.
; APPLICANT: Møller, Anette
; TITLE OF INVENTION: An Enzyme With Galactanase Activity
; FILE REFERENCE: 4686.204-US
; CURRENT APPLICATION NUMBER: US/09/137,855B
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 0233/96
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 0235/96
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: PCT/DK97/00092
; EARLIER FILING DATE: 1997-02-28
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Myceliophthora thermophila
; US-09-137-855-1

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 1050;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 798 CCAATGTGCTCGACACG 780

RESULT 23
US-09-347-819-5/C
; Sequence 5, Application US/09347819
; Patent No. 6184036
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Falco, S. Carl
; TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
; FILE REFERENCE: BB-1174-C
; CURRENT APPLICATION NUMBER: US/09/347,819
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/093,209
; EARLIER FILING DATE: July 17, 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1117
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (225)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (229)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (246)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (255)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (308)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (320)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1043)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1068)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1070)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1084)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1100)
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FEATURE:
NAME/KEY: unsure
LOCATION: (1114)
FEATURE:
NAME/KEY: unsure
LOCATION: (1116)
US-09-347-819-5

Query Match 52.6%; Score 10; DB 4; Length 1117;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
DB 769 CCAATGGGCCAAACCACG 751

RESULT 24
US-09-134-001C-1855/C
Sequence 1855, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1855
LENGTH: 1137
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1855

Query Match 52.6%; Score 10; DB 4; Length 1137;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
DB 683 CCAATAGCTCTATTCACG 665

RESULT 25
US-09-541-941B-27/C
Sequence 27, Application US/09541941B
Patent No. 6309840
GENERAL INFORMATION:
APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chui
APPLICANT: Ngao, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
TITLE OF INVENTION: FOR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-2A
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 1193
TYPE: DNA
ORGANISM: Pheretima Aspergillus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (100)..(100)
OTHER INFORMATION: n = a, t, c, g, or u
US-09-541-941B-27

Query Match 52.6%; Score 10; DB 4; Length 1193;
Best Local Similarity 52.6%; Pred. No. 4.7e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
DB 24 CCAATGGTAGGACGCACG 6

RESULT 26
US-08-286-819A-7
Sequence 7, Application US/08286819A
Patent No. 5871910
GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE

APPLICANT: COURVALIN, PATRICE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR

TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A

FILING DATE: 05-AUG-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

LOCATION: 215..1243
US-08-286-819A-7

Query Match 52.6%; Score 10; DB 2; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 961 CCAATTATATCAGCGCCACG 979

RESULT 27

US-08-286-819A-31
Sequence 31, Application US/08286819A
Patent No. 5871910

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEIDS, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 1347 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-236-819A-31

Query Match 52.6%; Score 10; DB 2; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 961 CCAATTATATCAGCGCCACG 979

RESULT 28

US-08-980-357-7
Sequence 7, Application US/08980357
Patent No. 6013508

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEIDS, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1347 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 215..1243
US-08-980-357-7

Query Match 52.6%; Score 10; DB 3; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Db 961 CCAATTATCAGCCGACG 979

RESULT 29
US-08-980-357-31
Sequence 31, Application US/08980357
Patent No. 6013508

GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C. S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819

FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990

ATTORNEY/AGENT INFORMATION:
NAME: OHLON, NO. 6013508man F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid

STRANDEDNESS: unknown
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-980-357-31

Query Match 52.6%; Score 10; DB 3; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
|||||
Db 961 CCAATTATCAGCCGACG 979

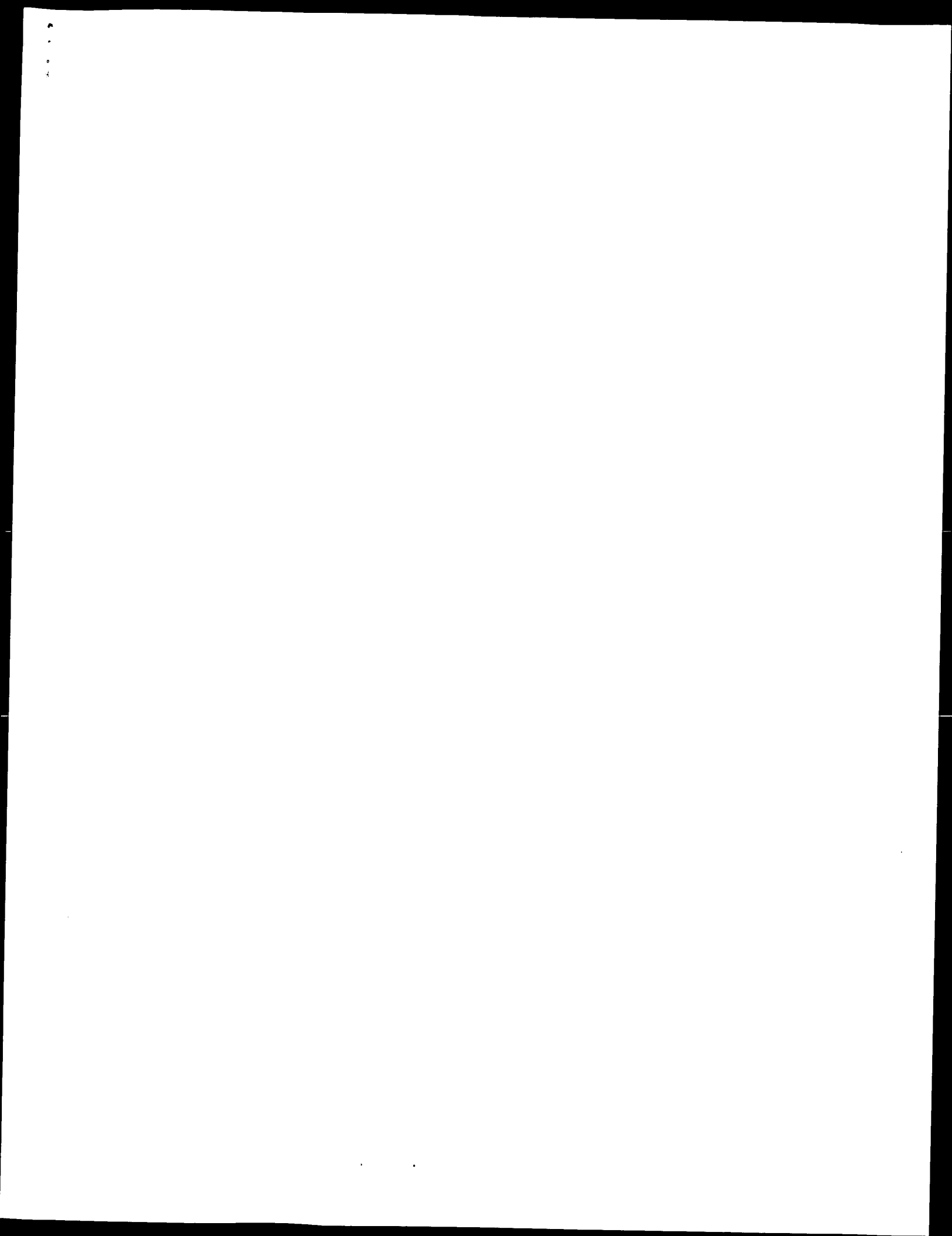
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US-09-134-001C-1389
Sequence 1389, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1389
LENGTH: 1377
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1389

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Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Search completed: November 16, 2002, 03:33:38
Job time : 50 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 01:20:22 ; Search time 2576 Seconds

(without alignments)
214.656 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 205640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

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4: gb_om:*

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_mus:*

33: em_htg_other:*

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35: em_htg_rtd:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	10	52.6	19 6 E28797	E28797 Endoplasmic
3	10	52.6	19 6 E28801	E28801 Endoplasmic
4	10	52.6	19 6 E28802	E28802 Endoplasmic
5	10	52.6	19 6 E28803	E28803 Endoplasmic
6	10	52.6	19 6 E28804	E28804 Endoplasmic
7	10	52.6	19 6 E28805	E28805 Endoplasmic
8	10	52.6	19 6 E28806	E28806 Endoplasmic
9	10	52.6	19 6 E28807	E28807 Endoplasmic
10	10	52.6	19 6 E28808	E28808 Endoplasmic
11	10	52.6	19 6 E28809	E28809 Endoplasmic
12	10	52.6	19 6 E44202	E44202 Endoplasmic
13	10	52.6	19 6 E44206	E44206 Endoplasmic
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15	10	52.6	19 6 E44208	E44208 Endoplasmic
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19	10	52.6	19 6 E44212	E44212 Endoplasmic
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21	10	52.6	19 6 E44214	E44214 Endoplasmic
22	10	52.6	24 6 AX443752	AX443752 Sequence
23	10	52.6	25 6 AX447733	AX447733 Sequence
24	10	52.6	29 6 E44234	E44234 Endoplasmic
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26	10	52.6	105 8 AF479941	AF479941 Saccharom
27	10	52.6	112 6 AX343726	AX343726 Sequence
28	10	52.6	122 6 E28800	E28800 Endoplasmic
29	10	52.6	122 6 E44205	E44205 Endoplasmic
30	10	52.6	125 14 AF271990	AF271990 Human ade
31	10	52.6	127 6 AX343728	AX343728 Sequence
32	10	52.6	136 6 AX033516	AX033516 Sequence
33	10	52.6	136 6 AX033517	AX033517 Sequence
34	10	52.6	142 6 AX033504	AX033504 Sequence
35	10	52.6	143 6 AX033505	AX033505 Sequence
36	10	52.6	143 6 HUMETG05	HUMETG05 Homo sapien
37	10	52.6	145 6 AX072778	AX072778 Sequence
38	10	52.6	149 6 AX033508	AX033508 Sequence
39	10	52.6	150 6 AX033507	AX033507 Sequence
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43	10	52.6	195 6 AX310584	AX310584 Sequence
44	10	52.6	204 6 AF229112S3	AF229114 Downingia
45	10	52.6	205 8 AX386623	AX386623 Sequence
46	10	52.6	210 6 AX439681	AX439681 Sequence
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49	10	52.6	220 6 BT010392	U10392 Bos taurus
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60	10	52.6	237 6 AX209173	AX209173 Sequence
61	10	52.6	244 8 AY020507	AY020507 Oryza sat
62	10	52.6	250 11 G31118	G31118 human STS S
63	10	52.6	255 9 HS8C1R	Z66326 H. sapiens C
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ALIGNMENTS

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RESULT 1
AX275341 19 bp DNA linear PAT 29-OCT-2001
LOCUS AX275341
DEFINITION Sequence 1 from Patent WO0171018.
ACCESSION AX275341
VERSION AX275341.1 GI:16547677
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hermonat,P.L., Mane,M. and Liu,Y.
TITLE Transferring products from skin by adeno-associated virus (aav) gene
JOURNAL Patent: WO 0171018-A 1 27-SEP-2001;
FEATURES
source THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
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Location/Qualifiers
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/db_xref="taxon:32644"
/note="glucose response element"
BASE COUNT 3 a 5 c 1 g 9 others
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QY 1 CCAATNNNNNNNNCCAG 19
Db 1 CCAATNNNNNNNNCCAG 19

RESULT 2
E28797 19 bp DNA linear PAT 18-JUN-2001
LOCUS E28797
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28797
VERSION E28797.1 GI:13020851
KEYWORDS JP 1999243959-A/1.
SOURCE unidentified.
ORGANISM unidentified.

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REFERENCE 1 (bases 1 to 19)
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 1 14-SEP-1999;
COMMENT HSP RESEARCH INST INC
OS Unidentified
PN JP 1999243959-A/1
PD 14-SEP-1999
PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FT enhancer
FEATURES
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BASE COUNT 3 a 5 c 1 g 9 others
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Query Match 52.6%: Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
Db 1 CCAATNNNNNNNNCCAG 19

RESULT 3
E28801 19 bp DNA linear PAT 18-JUN-2001
LOCUS E28801
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28801
VERSION E28801.1 GI:13020855
KEYWORDS JP 1999243959-A/5.
SOURCE
ORGANISM
REFERENCE
AUTHORS Mammalia,Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Hideo,Y., Hideki,Y. and Takashi,Y.
JOURNAL Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 5 14-SEP-1999;
FEATURES
source HSP RESEARCH INST INC
OS Homo sapiens (human)
PN JP 1999243959-A/5
PD 14-SEP-1999
PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
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CC Topology: Linear;
FH Key
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.8e+04;
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QY 1 CCAATNNNNNNNNCCAG 19

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DB 1 CCAATCGGCGGCTCCACG 19

RESULT 4
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LOCUS Endoplasmic reticulum stress-response regulatory element.

DEFINITION E28802
ACCESSION E28802.1 GI:13020856
VERSION JP 1999243959-A/6.
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.

REFERENCE
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE 1 (bases 1 to 19)
JOURNAL Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 6 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT
OS Mus sp. (mouse)
PN JP 1999243959-A/6
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453

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location/Qualifiers

BASE COUNT 4 a 8 c 5 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 1 CCAATCGGAGGCTCCACG 19

RESULT 5
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LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28803
ACCESSION E28803.1 GI:13020857
VERSION JP 1999243959-A/7.
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 7 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT
OS Rattus sp. (rat)
PN JP 1999243959-A/7
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K38/00, A61K48/00, C12N15/00,
A61K37/02

CC Strandedness: Double;
CC Topology: Linear;
FH key location/Qualifiers
FT enhancer 1. .19.
location/Qualifiers

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LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28804
ACCESSION E28804.1 GI:13020858
VERSION JP 1999243959-A/8.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE 1 (bases 1 to 19)
JOURNAL Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 8 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT
OS Homo sapiens (human)
PN JP 1999243959-A/8
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453

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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 1 CCAATCGGCGGCGCACGACG 19

RESULT 7
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LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28805
ACCESSION E28805.1 GI:13020859
VERSION JP 1999243959-A/9.
KEYWORDS
SOURCE Gallus sp.
ORGANISM Gallus sp.

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Db	1	CCAATCGGAAGGAGCCACG	19							

RESULT 9				
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LOCUS	E28807	19 bp	DNA	linear
DEFINITION	Endoplasmic reticulum stress-response regulatory element.			
ACCESSION	E28807			PAT 18-JUN-2001

ORGANISM
Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 19)	Hideo, Y., Hideki, Y. and Takashi, Y.	Endoplasmic reticulum stress-response regulatory element	
		Patent: JP 1999243959-A 11 14-SEP-1999;		
		HSP RESEARCH INST INC		
		OS Gallus sp. (chicken)		

PD	14-SEP-1999	JP	1998052453
PF	04-MAR-1998		
PR			

P1 HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K48/00, C12N15/00
PC A61K37/02
CC Strandedness: Double;
cc

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Best Local Similarity	52.6%;	Pred. No. 1.8e+04;		
Matches 10;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0;

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db 1 CCAATCGACGCCGCCAG 19

RESULT 10
E28808

Accession	Length	Type	Accession
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E28808		linear	
LOCUS			
DEFINITION			
ENDoplasmic reticulum stress-response regulatory element.			
ACCESION			

EXTENSION
KEYWORDS
SOURCE
Homo sapiens
JP 1999243959-A/12.
E28808.1 GI:13020862

ORGANISM
 homo sapiens
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae

1 (bases 1 to 19)
Hideo, Y., Hideki, Y. and Takashi, Y.
Endoplasmic reticulum stress-response regulatory element

OS Homo sapiens (human)
HSP RESEARCH INST INC
RECORD OF 1000240000 A
COMMENT

PD	14-SEP-1999
PF	04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FT enhancer
Location/Qualifiers
1.19
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 5 a 6 c 5 g 3 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATGATGGTGCACCACG 19

RESULT 11
E28809 19 bp DNA linear PAT 18-JUN-2001
LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28809
ACCESSION E28809 GI:13020863
VERSION E28809.1
KEYWORDS JP 1999243959-A/13.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 13 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Mus sp. (mouse)
PN JP 1999243959-A/13
PD 14-SEP-1999
PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FT enhancer
Location/Qualifiers
1.19
/organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 5 a 6 c 6 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATGATGGTGCACCACG 19

RESULT 12
E44202 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44202
ACCESSION E44202 GI:18633455
VERSION

KEYWORDS JP 2001054391-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hajl,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 1 27-FEB-2001;
HSP RESEARCH INST INC
COMMENT OS Artificial Sequence
PN JP 2001054391-A/1
PD 27-FEB-2001
PR 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
(C12N15/00, PC C12R1:91)
CC
FH Key
FT source
Location/Qualifiers
1.19
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 5 c 1 g 1 t 9 others
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATNNNNNNNNCCACG 19

RESULT 13
E44206 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44206
ACCESSION E44206 GI:18633459
VERSION E44206.1
KEYWORDS JP 2001054391-A/5.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hajl,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 5 27-FEB-2001;
HSP RESEARCH INST INC
COMMENT OS Homo sapiens (human)
PN JP 2001054391-A/5
PD 27-FEB-2001
PR 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
(C12N15/00, PC C12R1:91)
CC
FH Key
FT source
Location/Qualifiers
1.19
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 9 c 5 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

RESULT 14
E44207 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44207
VERSION E44207.1 GI:18633460
KEYWORDS JP 2001054391-A/6.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 6 27-FEB-2001;
HSP RESEARCH INST INC

OS Mus sp. (murine)
PN JP 2001054391-A/6
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR

PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..19
Location/Qualifiers
1..19
/organism="Mus sp. (murine)"
/db_xref="taxon:10095"

BASE COUNT 4 a 8 c 5 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

RESULT 15
E44208 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44208
VERSION E44208.1 GI:18633461
KEYWORDS JP 2001054391-A/7.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 7 27-FEB-2001;
HSP RESEARCH INST INC

OS Rattus sp. (rat)
COMMENT

PN JP 2001054391-A/7
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR

PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..19
Location/Qualifiers
1..19
/organism="Rattus sp. (rat)"
/db_xref="taxon:10118"

BASE COUNT 4 a 8 c 5 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

RESULT 16
E44209 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44209
VERSION E44209.1 GI:18633462
KEYWORDS JP 2001054391-A/8.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 8 27-FEB-2001;
HSP RESEARCH INST INC

OS Homo sapiens (human)
PN JP 2001054391-A/8
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR

PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..19
Location/Qualifiers
1..19
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"

BASE COUNT 4 a 10 c 4 g 1 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

RESULT 17
E44210 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44210
ACCESSION E44210.1 GI:18633463
VERSION JP 2001054391-A/9.
KEYWORDS Gallus sp.
SOURCE Gallus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 9 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Gallus sp. (chicken)
PN JP 2001054391-A/9
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC

FEATURES
source Location/Qualifiers
FT 1..19
FT source /organism='Gallus sp. (chicken)'.
1..19
/organism='Gallus sp. "
/db_xref='taxon:9036"
BASE COUNT 5 a 7 c 6 g 1 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATGGAGCGCACCCACG 19

RESULT 18
E44211 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44211
ACCESSION E44211.1 GI:18633464
VERSION JP 2001054391-A/10.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 10 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Homo sapiens (human)
PN JP 2001054391-A/10
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC

FEATURES
FH key Location/Qualifiers
FT source

FT source 1..19
/organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
FT 1..19
/organism='Homo sapiens "
/db_xref='taxon:9606"
BASE COUNT 6 a 6 c 6 g 1 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGAGCGCGCACCG 19

RESULT 19
E44212 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44212
ACCESSION E44212.1 GI:18633465
VERSION JP 2001054391-A/11.
KEYWORDS Gallus sp.
SOURCE Gallus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 11 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Gallus sp. (chicken)
PN JP 2001054391-A/11
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91)
CC

FEATURES
FH key Location/Qualifiers
FT source 1..19
/organism='Gallus sp. (chicken)'.
1..19
/organism='Gallus sp. "
/db_xref='taxon:9036"
BASE COUNT 4 a 9 c 5 g 1 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGAGCGCGCACCG 19

RESULT 20
E44213 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44213
ACCESSION E44213.1 GI:18633466
VERSION JP 2001054391-A/12.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Hajj, K., Yoshida, H., Mori, K., Yanaqi, H. and Yura, T.
 TITLE Endoplasmic reticulum stress transcription factor
 JOURNAL Patent: JP 2001054391-A 12 27-FEB-2001;
 HSP RESEARCH INST INC

COMMENT

OS Homo sapiens (human)
 PN JP 2001054391-A/12
 PD 27-FEB-2001
 PR 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
 TAKASHI YURA
 PC C12N15/09, C12P21/02//((C12N15/09, C12R1:91), C12N15/00,
 (C12N15/00, PC C12R1:91)
 CC
 FH key Location/Qualifiers
 FT source 1..19 /organism='Homo sapiens (human)'

FEATURES

source Location/Qualifiers
 1..19 /organism='Homo sapiens'

BASE COUNT 5 a 6 c 5 g 3 t
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 1 CCAATGATGTCGACACG 19

RESULT 21
 LOCUS E44214 19 bp DNA linear PAT 31-JAN-2002
 DEFINITION Endoplasmic reticulum stress transcription factor.
 ACCESSION E44214
 E44214.1 GI:18633467
 JP 2001054391-A/13.
 KEYWORDS Mus sp.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 AUTHORS Hajj, K., Yoshida, H., Mori, K., Yanaqi, H. and Yura, T.
 TITLE Endoplasmic reticulum stress transcription factor
 JOURNAL Patent: JP 2001054391-A 13 27-FEB-2001;
 HSP RESEARCH INST INC

OS Mus sp. (murine)
 PN JP 2001054391-A/13
 PD 27-FEB-2001
 PR 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
 TAKASHI YURA
 PC C12N15/09, C12P21/02//((C12N15/09, C12R1:91), C12N15/00,
 (C12N15/00, PC C12R1:91)
 CC
 FH key Location/Qualifiers
 FT source 1..19 /organism='Mus sp. (murine)'

FEATURES
 source Location/Qualifiers
 1..19 /organism='Mus sp.'

BASE COUNT 5 a 6 c 6 g 2 t
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 1 CCAATGATGTCGACACG 19

RESULT 22
 LOCUS AX443752/c 24 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 207 from Patent WO0216649.
 ACCESSION AX443752
 VERSION AX443752.1 GI:21691030
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 0216649-A 207 28-FEB-2002;
 Illumina, Inc. (US)

FEATURES
 source Location/Qualifiers
 1..24 /organism='synthetic construct'

BASE COUNT 4 a 5 c 9 g 6 t
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 24;
 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 23 CCAATATTTACGTGACACG 5

RESULT 23
 LOCUS AX447733/c 25 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 4188 from Patent WO0216649.
 ACCESSION AX447733
 VERSION AX447733.1 GI:21696632
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 0216649-A 4188 28-FEB-2002;
 Illumina, Inc. (US)

FEATURES
 source Location/Qualifiers
 1..25 /organism='synthetic construct'

BASE COUNT 4 a 5 c 9 g 7 t
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 25;
 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 24 CCAATATTTACGTGACACG 6

RESULT 24

E44234		29 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	E44234				
DEFINITION	Endoplasmic reticulum stress transcription factor.				
ACCESSION	E44234				
VERSION	E44234.1	GI:18633487			
KEYWORDS	JP 2001054391-A/33.				
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 29)				
AUTHORS	Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.				
TITLE	Endoplasmic reticulum stress transcription factor				
JOURNAL	Patent: JP 2001054391-A 33 27-FEB-2001;				
	HSP RESEARCH INST INC				
COMMENT	OS Artificial Sequence				
	PN JP 2001054391-A/33				
	PD 27-FEB-2001				
	PF 11-NOV-1999 JP 1999321743				
	PR KYOJUKU HAJI,HIDRO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI				
	PI TAKASII YURA				
	PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,				
	(C12N15/00, PC C12R1:91)				
FEATURES	CC				
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	Key Location/Qualifiers				
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	location/Qualifiers				
	1..29				
	/organism='synthetic construct'				
	/db_xref='taxon:32630'				
BASE COUNT	5 a 13 c 7 g 4 t				
ORIGIN					
Query Match	52.6%; Score 10; DB 6; Length 29;				
Best Local Similarity	52.6%; Pred. No. 1.8e+04;				
Matches 10; Conservative	0; Mismatches 9; Indels 0; Gaps 0;				
OY	1 CCAATNNNNNNNCCACG 19				
Db	7 CCAATCGGGCTCCACG 25				
RESULT 25					
HUMCG3A02/c		99 bp	DNA	linear	PRI 01-NOV-1994
LOCUS	HUMCG3A02				
DEFINITION	Human alpha-1(III) collagen gene, exon 22.				
ACCESSION	M10797				
VERSION	M10797.1	GI:180398			
KEYWORDS	alpha-1 type III collagen.				
SEGMENT	2 of 12				
SOURCE	Human DNA, libraries of A.Bank and T.Manatis, clones IdF-[4,7].				
ORGANISM	Human sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
REFERENCE	1 (bases 1 to 99)				
AUTHORS	Chu,M.L., Well,L.D., de Wet,W., Bernard,M., Sippola,M. and Ramirez,F				
TITLE	Isolation of cDNA and genomic clones encoding human pro-alpha 1				
	(III) collagen. Partial characterization of the 3' end region of				
	the gene				
JOURNAL	J Biol. Chem. 260 (7), 4357-4363 (1985)				
MEDLINE	85157600				
PUBMED	2579949				
FEATURES					
source	location/Qualifiers				
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	/db_xref='taxon:9606'				
	/cell_type='fibroblast'				
	/tissue_idb='Of A.Bank and T.Manatis'				
	<1..>99				
	/gene='COL3A1'				
	/note='exon 22'				
	/codon_start=1				
CDS					

BASE COUNT		17 a 25 c 39 g 18 t		About 1.0 kb after segment 1; chromosome 2q31-q32.3.	
ORIGIN					
Query Match	52.6%;	Score 10;	DB 9;	Length 99;	
Best Local Similarity	52.6%;	Pred. No. 1.8e+04;			
Matches	10;	Conservative	0;	Mismatches	9;
				Indels	0;
				Gaps	0;
OY	1	CCAAATNNNNNNNNCCACG	19		
Db	43	CCAATCCAGGAGCTCCACG	25		
RESULT 26					
LOCUS	AF479941	105 bp	DNA	linear	PLN 20-FEB-2002
DEFINITION	Saccharomyces cerevisiae YDL025W-A gene, complete cds.				
ACCESSION	AF479941				
VERSION	AF479941.1	GI:18767077			
KEYWORDS	Saccharomyces cerevisiae.				
SOURCE	Saccharomyces cerevisiae				
ORGANISM	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetes.				
REFERENCE	1 (bases 1 to 105)				
AUTHORS	Kumar,A., Harrison,P.M., Cheung,K.H., Ian,N., Echols,N., Bertonc,P., Miller,P., Gerstein,M.B. and Snyder,M.				
TITLE	An integrated approach for finding overlooked genes in yeast				
JOURNAL	Nat. Biotechnol. 20 (1), 58-63 (2002)				
MEDLINE	21624570				
PUBMED	11753363				
REFERENCE	2 (bases 1 to 105)				
AUTHORS	Kumar,A., Paul,H.M., Cheung,K.H., Ian,N., Echols,N., Bertonc,P., Miller,P., Gerstein,M.B. and Snyder,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-FEB-2002) MCD Biology, Yale University, P.O. Box 208103, New Haven, CT 06520-8103, USA				
FEATURES	Location/Qualifiers				
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				Indels	0;
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RESULT 27					
LOCUS	AX343726	112 bp	DNA	linear	PAT 01-FEB-2002
DEFINITION	Sequence 1 from Patent W00200706.				
ACCESSION	AX343726				

VERSION AX343726.1 GI:18491804
KEYWORDS
SOURCE
ORGANISM Pseudacanthotermes spiniger.
Pseudacanthotermes spiniger
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Termitidae;
Macrotermittinae; Pseudacanthotermes.
REFERENCE
AUTHORS Lambert, M., Bulet, P., Latorse, M.P. and Hoffmann, J.
TITLE Antimicrobial peptides of the family of defensins, polynucleotides
encoding said peptides, transformed vectors and organisms
containing them
JOURNAL Patent: WO 0200706-A 1 03-JAN-2002;
Rhubio (FR)
FEATURES
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Db 12 CCAATCTTGTGGCCACG 30
RESULT 28
E28800
LOCUS E28800 122 bp DNA linear PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION E28800
VERSION E28800.1 GI:13020854
KEYWORDS JP 1999243959-A/4.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Hideo, Y., Hideki, T. and Takashi, Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 4 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT
OS Homo sapiens (human)
PN JP 1999243959-A/4
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR
PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key location/Qualifiers
FT enhancer 15..33
FT enhancer 47..65
FT enhancer 80..98
FT TATA signal 116..122.
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source location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 22 a 35 c 48 g 17 t
ORIGIN

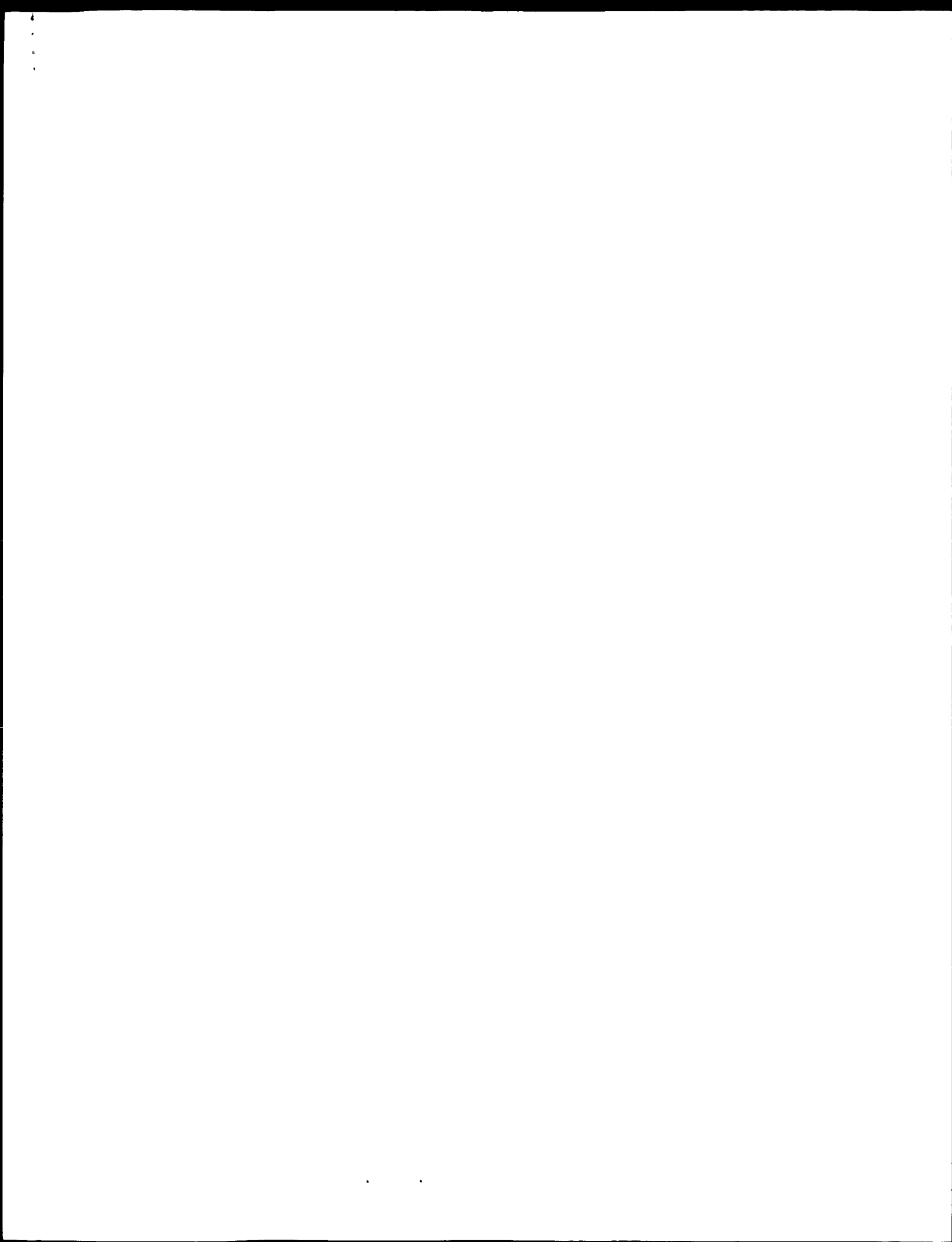
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Db 80 CCAATCGCGCGCTCCACG 98
RESULT 29
E44205
LOCUS E44205 122 bp DNA linear PAT 31-JAN-2002
DEFINITION Endoplasmic reticulum stress transcription factor.
ACCESSION E44205
VERSION E44205.1 GI:18633458
KEYWORDS JP 2001054391-A/4.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Hajt, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 4 27-FEB-2001;
HSP RESEARCH INST INC
COMMENT
OS Homo sapiens (human)
PN JP 2001054391-A/4
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR
PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
C12N15/00, PC C12R1:91
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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
|||||
Db 80 CCAATCGCGCGCTCCACG 98
RESULT 30
AF271990
LOCUS AF271990/3 125 bp DNA linear VRL 02-JUN-2001
DEFINITION Human adenovirus type 19p strain 587 inverted terminal repeat,
partial sequence.
ACCESSION AF271990
VERSION AF271990.1 GI:14279590
KEYWORDS
SOURCE human adenovirus type 19p.
ORGANISM human adenovirus type 19p.
REFERENCE
AUTHORS Blusch, J.H., Deryckere, F., Windheim, M., Ruzsics, Z., Arndberg, N.,
Adrian, T. and Burgerl, H.G.
TITLE E3/49K: A Novel Early Region 3 Protein Specifically Expressed By
JOURNAL Adenoviruses of Subgroup D
REFERENCE Unpublished
2 (bases 1 to 125)

AUTHORS Ruzsics, Z. and Burgert, H.G.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2000) Dep. of Virology, Gene Center-Max V.
 Pettenkofer Inst., Feodor-Lynen-Str. 25, Muenchen 81377, Germany

FEATURES
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 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCAGC 19
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 DB 86 CCAATCAACGACGACCAGC 68

Search completed: November 16, 2002, 02:59:16
 Job time : 2579 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: November 16, 2002, 01:16:17 : Search time 257 Seconds
(without alignments)
166.490 Million cell updates/sec

Title: US-09-606-804-1
Perfect score: 19
Sequence: 1 ccaatnnnnnnnnccacg 19
Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478
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Listing first 90 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	52.6	19	20	AA225631	Endoplasmic reticu
2	52.6	19	20	AA225632	Endoplasmic reticu
3	52.6	19	20	AA225633	Endoplasmic reticu
4	52.6	19	20	AA225634	Endoplasmic reticu
5	52.6	19	20	AA225635	Endoplasmic reticu
6	52.6	19	20	AA225636	Endoplasmic reticu
7	52.6	19	20	AA225637	Endoplasmic reticu
8	52.6	19	20	AA225638	Endoplasmic reticu
9	52.6	19	20	AA225639	Endoplasmic reticu

10	52.6	19	20	AA225640	Endoplasmic reticu
11	52.6	19	21	AAA28570	GRP78 promoter ERS
12	52.6	19	21	AAA28571	GRP78 promoter ERS
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16	52.6	19	21	AAA28575	GRP78 promoter ERS
17	52.6	19	21	AAA28576	GRP78 promoter ERS
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19	52.6	19	21	AAA28578	GRP78 promoter ERS
20	52.6	19	21	AAA28579	GRP78 promoter ERS
21	52.6	19	22	AA170001	Calreticulin promo
22	52.6	19	22	AA170001	Calreticulin promo
23	52.6	19	22	AA170001	Calreticulin promo
24	52.6	19	22	AA170001	Calreticulin promo
25	52.6	19	22	AA170001	Calreticulin promo
26	52.6	19	22	AA170001	Calreticulin promo
27	52.6	19	22	AA170001	Calreticulin promo
28	52.6	19	22	AA170001	Calreticulin promo
29	52.6	19	22	AA170001	Calreticulin promo
30	52.6	19	22	AA170001	Calreticulin promo
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44	52.6	19	22	AA170001	Calreticulin promo
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81	52.6	19	22	AA170001	Calreticulin promo
82	52.6	19	22	AA170001	Calreticulin promo

XX 14-SEP-1999.
 PD 04-MAR-1998; 98JP-0052453.
 XX 04-MAR-1998; 98JP-0052453.
 PR 04-MAR-1998; 98JP-0052453.
 XX (HSPK-) HSP KENKYUSHO KK.
 PA WPI: 1999-603708/52.
 XX
 DR New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 PT cells
 XX
 PS Example 1: Fig 3: 25pp; Japanese.
 XX
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum used for stress
 CC competence of endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC growth and induction of apoptosis of cancer cells, and improvement of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 CC autoantibody formation. AA25632 to AA25657 represent elements used in
 CC an example from the present invention.
 CC
 SQ Sequence 19 BP: 4 A; 8 C; 5 G; 2 T; 0 other;
 Query Match 52.6%; Score 10; DB 20; Length 19;
 Best local Similarity 52.6%; Pred. No. 1.4e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNN NNNCCACG 19
 Db 1 CCAATCGAGGCGCTCCACG 19
 ||||| |||||
 RESULT 4
 AA25634
 ID AA25634 standard: DNA: 19 BP.
 XX AA25634;
 AC
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:7.
 XX
 KM Endoplasmic reticulum; ER; stress competence; control element;
 KM inhibition; growth; apoptosis; cancer; autoimmune disease;
 XX cystic fibrosis; ds.
 XX
 OS Rattus sp.
 XX
 PN JP11243959-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 04-MAR-1998; 98JP-0052453.
 XX
 PR 04-MAR-1998; 98JP-0052453.
 XX
 PA (HSPK-) HSP KENKYUSHO KK.
 XX
 DR WPI: 1999-603708/52.
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 PT cells

XX Example 1: Fig 3: 25pp; Japanese.
 PS
 XX
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum used for stress
 CC competence of endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC growth and induction of apoptosis of cancer cells, and improvement of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 CC autoantibody formation. AA25632 to AA25657 represent elements used in
 CC an example from the present invention.
 CC
 SQ Sequence 19 BP: 4 A; 8 C; 5 G; 2 T; 0 other;
 Query Match 52.6%; Score 10; DB 20; Length 19;
 Best local Similarity 52.6%; Pred. No. 1.4e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNN NNNCCACG 19
 Db 1 CCAATCGAGGCGCTCCACG 19
 ||||| |||||
 RESULT 5
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 ID AA25635 standard: DNA: 19 BP.
 XX AA25635;
 AC
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:8.
 XX
 KM Endoplasmic reticulum; ER; stress competence; control element;
 KM inhibition; growth; apoptosis; cancer; autoimmune disease;
 XX cystic fibrosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP11243959-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 04-MAR-1998; 98JP-0052453.
 XX
 PR 04-MAR-1998; 98JP-0052453.
 XX
 PA (HSPK-) HSP KENKYUSHO KK.
 XX
 DR WPI: 1999-603708/52.
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 PT cells
 XX
 PS Example 1: Fig 3: 25pp; Japanese.
 XX
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCACG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum used for stress
 CC competence of endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC growth and induction of apoptosis of cancer cells, and improvement of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of

CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
DB 1 CCAATCGCGCCGACCACG 19

RESULT 6
AA25636
ID AA25636 standard; DNA; 19 BP.

XX AA25636;

XX 23-DEC-1999 (first entry)

DE Endoplasmic reticulum stress competence control element SEQ ID NO:9.

XX Endoplasmic reticulum; ER; stress competence; control element;

KW inhibition; growth; apoptosis; cancer; autoimmune disease;

KW cystic fibrosis; ds.

XX Gallus sp.

XX JP11243959-A.

XX 14-SEP-1999.

XX 04-MAR-1998; 98JP-0052453.

XX 04-MAR-1998; 98JP-0052453.

XX (HSPK-) HSP KENKYUSHO KK.

XX WPI; 1999-603708/52.

XX New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells

PS Example 1; Fig 3; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.

XX Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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DB 1 CCAATGCGAGCCGACCACG 19

RESULT 7
AA25637
ID AA25637 standard; DNA; 19 BP.

XX AA25637;

XX 23-DEC-1999 (first entry)

DE Endoplasmic reticulum stress competence control element SEQ ID NO:10.

XX Endoplasmic reticulum; ER; stress competence; control element;

KW inhibition; growth; apoptosis; cancer; autoimmune disease;

KW cystic fibrosis; ds.

XX Homo sapiens.

XX JP11243959-A.

XX 14-SEP-1999.

XX 04-MAR-1998; 98JP-0052453.

XX 04-MAR-1998; 98JP-0052453.

XX (HSPK-) HSP KENKYUSHO KK.

XX WPI; 1999-603708/52.

XX New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells

PS Example 1; Fig 3; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.

XX Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
DB 1 CCAATCGGAGAGCCGACCACG 19

RESULT 8
AA25638
ID AA25638 standard; DNA; 19 BP.

XX AA25638;

XX 23-DEC-1999 (first entry)

DE Endoplasmic reticulum stress competence control element SEQ ID NO:11.

XX Endoplasmic reticulum; ER; stress competence; control element;

KW inhibition; growth; apoptosis; cancer; autoimmune disease;

KW cystic fibrosis; ds.

XX

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OS      Gallus sp.
XX      JP11243959-A.
XX      14-SEP-1999.
XX      04-MAR-1998; 98JP-0052453.
XX      04-MAR-1998; 98JP-0052453.
XX      (HSPK-) HSP KENKYUSHO KK.
XX      WPI: 1999-603708/52.
XX      PT New control element for stress competence of endoplasmic reticulum -
XX      PT useful for inhibition of growth and induction of apoptosis in cancer
XX      cells
XX      Example 1: Fig 3; 25pp; Japanese.
XX      CC The present invention specifically claims an element shown by: (A) a
XX      CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
XX      CC transcription with stress on endoplasmic reticulum used for stress
XX      CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX      CC having transcription inducing activity with stress on endoplasmic
XX      CC reticulum containing the above mentioned element, optionally further
XX      CC containing a promoter DNA; and (2) a vector containing the element
XX      CC optionally with the DNA. The element can be used for the inhibition of
XX      CC growth and induction of apoptosis of cancer cells, and improvement of
XX      CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX      CC antibody formation. AA225632 to AA225657 represent elements used in
XX      CC an example from the present invention.
XX      SQ Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other:
XX      Query Match 52.6%; Score 10; DB 20; Length 19;
XX      Best Local Similarity 52.6%; Pred. No. 1.4e+03;
XX      Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX      OY 1 CCAATNNNNNNNNCCACG 19
XX      1 CCAATGATGTCGACCCACG 19
XX      DB 1 CCAATGATGTCGACCCACG 19
XX      RESULT 9
XX      ID AA225639 standard; DNA: 19 BP.
XX      AC AA225639;
XX      DT 23-DEC-1999 (first entry)
XX      DE Endoplasmic reticulum stress competence control element SEQ ID NO:12.
XX      KW Endoplasmic reticulum; ER; stress competence; control element;
XX      KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX      KW cystic fibrosis; ds.
XX      OS Homo sapiens.
XX      PN JP11243959-A.
XX      PD 14-SEP-1999.
XX      PF 04-MAR-1998; 98JP-0052453.
XX      PR 04-MAR-1998; 98JP-0052453.
XX      PA (HSPK-) HSP KENKYUSHO KK.
XX      WPI: 1999-603708/52.

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XX      PT New control element for stress competence of endoplasmic reticulum -
XX      PT useful for inhibition of growth and induction of apoptosis in cancer
XX      cells
XX      Example 1: Fig 3; 25pp; Japanese.
XX      CC The present invention specifically claims an element shown by: (A) a
XX      CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
XX      CC sequence having replaced 1-3 bases with the other base(s), which induces
XX      CC transcription with stress on endoplasmic reticulum used for stress
XX      CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX      CC having transcription inducing activity with stress on endoplasmic
XX      CC reticulum containing the above mentioned element, optionally further
XX      CC containing a promoter DNA; and (2) a vector containing the element
XX      CC optionally with the DNA. The element can be used for the inhibition of
XX      CC growth and induction of apoptosis of cancer cells, and improvement of
XX      CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
XX      CC antibody formation. AA225632 to AA225657 represent elements used in
XX      CC an example from the present invention.
XX      SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other:
XX      Query Match 52.6%; Score 10; DB 20; Length 19;
XX      Best Local Similarity 52.6%; Pred. No. 1.4e+03;
XX      Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX      OY 1 CCAATNNNNNNNNCCACG 19
XX      1 CCAATGATGTCGACCCACG 19
XX      DB 1 CCAATGATGTCGACCCACG 19
XX      RESULT 10
XX      ID AA225640 standard; DNA: 19 BP.
XX      AC AA225640;
XX      DT 23-DEC-1999 (first entry)
XX      DE Endoplasmic reticulum stress competence control element SEQ ID NO:13.
XX      KW Endoplasmic reticulum; ER; stress competence; control element;
XX      KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX      KW cystic fibrosis; ds.
XX      OS Mus sp.
XX      PN JP11243959-A.
XX      PD 14-SEP-1999.
XX      PF 04-MAR-1998; 98JP-0052453.
XX      PR 04-MAR-1998; 98JP-0052453.
XX      PA (HSPK-) HSP KENKYUSHO KK.
XX      WPI: 1999-603708/52.
XX      DR Homo sapiens.
XX      PN JP11243959-A.
XX      PD 14-SEP-1999.
XX      PF 04-MAR-1998; 98JP-0052453.
XX      PR 04-MAR-1998; 98JP-0052453.
XX      PA (HSPK-) HSP KENKYUSHO KK.
XX      WPI: 1999-603708/52.
XX      PT New control element for stress competence of endoplasmic reticulum -
XX      PT useful for inhibition of growth and induction of apoptosis in cancer
XX      cells
XX      Example 1: Fig 3; 25pp; Japanese.
XX      CC The present invention specifically claims an element shown by: (A) a
XX      CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
XX      CC sequence having replaced 1-3 bases with the other base(s), which induces
XX      CC transcription with stress on endoplasmic reticulum used for stress
XX      CC competence of endoplasmic reticulum. Also described are: (1) a DNA
XX      CC having transcription inducing activity with stress on endoplasmic
XX      CC reticulum containing the above mentioned element, optionally further
XX      CC containing a promoter DNA; and (2) a vector containing the element

```

optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AA25632 to AA25657 represent elements used in an example from the present invention.

Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 CCAATNNNNNNNNCCACG 19
1 CCAATGAGGCTCGACGACG 19

RESULT 11
AAA28570 standard; DNA: 19 BP.

AAA28570;

29-AUG-2000 (first entry)

GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum stress; ER; transcription factor;

transcription; regulatory element; ERSE; bZIP; chaperone; treatment;

prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;

cystic fibrosis; ulcer; gene therapy; recombinant gene; human;

gene expression; GRP; glucose regulated protein; promoter; ss.

Homo sapiens.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI; 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)

for controlling expression of endoplasmic reticulum chaperone, useful

for treating cancers, arteriosclerosis, cystic fibrosis, ischemic

diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)

capable of regulating transcription inducing activity exhibited by an

element (ERSE) can be used in a method for controlling expression of

an endoplasmic reticulum chaperone. The method comprises expressing

bZIP. The method can be used for expression of a foreign protein by

positively regulating expression of an endoplasmic reticulum

chaperone gene. bZIP is useful for controlling the expression of

endoplasmic reticulum chaperone either positively or negatively in

cells and therefore is useful for treatment or prophylaxis of

cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,

wounds and ulcers. bZIP also maintains the correct conformation of

the endoplasmic reticulum chaperone and thereby increases the

expression of a foreign protein. This sequence taken from the

glucose regulating protein (GRP) promoter GRP78 contains an ERSE like

sequence.

Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;

Query Match 52.6%; Score 10; DB 21; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 CCAATNNNNNNNNCCACG 19
1 CCAATCGGCGCTCGACG 19

RESULT 12
AAA28571 standard; DNA: 19 BP.

AAA28571;

29-AUG-2000 (first entry)

GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum stress; ER; transcription factor;

transcription; regulatory element; ERSE; bZIP; chaperone; treatment;

prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;

cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;

gene expression; GRP; glucose regulated protein; promoter; ss.

Mus musculus.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI; 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)

for controlling expression of endoplasmic reticulum chaperone, useful

for treating cancers, arteriosclerosis, cystic fibrosis, ischemic

diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)

capable of regulating transcription inducing activity exhibited by an

element (ERSE) can be used in a method for controlling expression of

an endoplasmic reticulum chaperone. The method comprises expressing

bZIP. The method can be used for expression of a foreign protein by

positively regulating expression of an endoplasmic reticulum

chaperone gene. bZIP is useful for controlling the expression of

endoplasmic reticulum chaperone either positively or negatively in

cells and therefore is useful for treatment or prophylaxis of

cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,

wounds and ulcers. bZIP also maintains the correct conformation of

the endoplasmic reticulum chaperone and thereby increases the

expression of a foreign protein. This sequence taken from the

glucose regulating protein (GRP) promoter GRP78 contains an ERSE like

sequence.

OY 1 CCAATNNNNNNNNCCACG 19
 |||||
 DB 1 CCAATCGGAGCGCTCCACG 19

RESULT 13

AAA28572 standard; DNA: 19 BP.

AAA28572:

29-AUG-2000 (first entry)

GRP78 promoter ERSEL-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
 transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 cystic fibrosis; ulcer; gene therapy; recombinant gene; rat;
 gene expression; GRP; glucose regulated protein; promoter; ss.

Rattus rattus.

MO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
 for controlling expression of endoplasmic reticulum chaperone, useful
 for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
 capable of regulating transcription inducing actively exhibited by an
 element (ERSE) can be used in a method for controlling expression of
 an endoplasmic reticulum chaperone. The method comprises expressing
 bZIP. The method can be used for expression of a foreign protein by
 positively regulating expression of an endoplasmic reticulum
 chaperone gene. bZIP is useful for controlling the expression of
 endoplasmic reticulum chaperone either positively or negatively in
 cells and therefore is useful for treatment or prophylaxis of
 cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 wounds and ulcers. bZIP also maintains the correct conformation of
 the endoplasmic reticulum chaperone and thereby increases the
 expression of a foreign protein. This sequence taken from the
 glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
 sequence.

Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||
 DB 1 CCAATCGGAGCGCTCCACG 19

RESULT 14

AAA28573 standard; DNA: 19 BP.

AAA28573:

29-AUG-2000 (first entry)

GRP94 promoter ERSEL-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
 transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 gene expression; GRP; glucose regulated protein; promoter; ss.

Homo sapiens.

MO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
 for controlling expression of endoplasmic reticulum chaperone, useful
 for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
 capable of regulating transcription inducing actively exhibited by an
 element (ERSE) can be used in a method for controlling expression of
 an endoplasmic reticulum chaperone. The method comprises expressing
 bZIP. The method can be used for expression of a foreign protein by
 positively regulating expression of an endoplasmic reticulum
 chaperone gene. bZIP is useful for controlling the expression of
 endoplasmic reticulum chaperone either positively or negatively in
 cells and therefore is useful for treatment or prophylaxis of
 cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 wounds and ulcers. bZIP also maintains the correct conformation of
 the endoplasmic reticulum chaperone and thereby increases the
 expression of a foreign protein. This sequence taken from the
 glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 sequence.

Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||

DB 1 CCAATCGGAGCGCTCCACG 19

RESULT 15

AAA28574 standard; DNA: 19 BP.

AAA28574:

29-AUG-2000 (first entry)

XX GRP94 promoter ERSE1-like sequence.

DE Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Gallus domesticus.

XX WO200029429-A2.

XX 25-MAY-2000.

XX 12-NOV-1999; 99WO-JP06305.

XX 13-NOV-1998; 98JP-0324227.

XX 09-JUN-1999; 99JP-0163112.

XX (HSPR-) HSP RES INST INC.

PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

DR WPI; 2000-387736/33.

XX New endoplasmic reticulum stress transcription factor (known as bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers

XX Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP)
 CC capable of regulating transcription inducing activity exhibited by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum
 CC chaperone gene. bZIP is useful for controlling the expression of
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bZIP also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 CC sequence.

XX Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;

XX Query Match 52.6%; Score 10; DB 21; Length 19;
 XX Best Local Similarity 52.6%; Pred. No. 1.4e+03;

XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

XX 1 CCAATNNNNNNNNCCACG 19
 XX 1 CCAATGGAGCGCACACG 19

XX RESULT 16

XX AAA28575

XX ID AAA28575 standard; DNA; 19 BP.

XX AAA28575;

XX 29-AUG-2000 (first entry)

XX GRP94 promoter ERSE3-like sequence.

XX Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;

KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Homo sapiens.

XX WO200029429-A2.

XX 25-MAY-2000.

XX 12-NOV-1999; 99WO-JP06305.

XX 13-NOV-1998; 98JP-0324227.

XX 09-JUN-1999; 99JP-0163112.

XX (HSPR-) HSP RES INST INC.

PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

DR WPI; 2000-387736/33.

XX New endoplasmic reticulum stress transcription factor (known as bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers

XX Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP)
 CC capable of regulating transcription inducing activity exhibited by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum
 CC chaperone gene. bZIP is useful for controlling the expression of
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bZIP also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 CC sequence.

XX Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;

XX Query Match 52.6%; Score 10; DB 21; Length 19;
 XX Best Local Similarity 52.6%; Pred. No. 1.4e+03;

XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

XX 1 CCAATNNNNNNNNCCACG 19
 XX 1 CCAATCGAAGAGCCACG 19

XX RESULT 17

XX AAA28576

XX ID AAA28576 standard; DNA; 19 BP.

XX AAA28576;

XX 29-AUG-2000 (first entry)

XX GRP94 promoter ERSE3-like sequence.

XX Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Gallus domesticus.

XX WO200029429-A2.

XX 25-MAY-2000.
XX 12-NOV-1999; 99WO-JP06305.
XX 13-NOV-1998; 98JP-0324227.
PR 09-JUN-1999; 99JP-0163112.
XX (HSPR-) HSP RES INST INC.
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI: 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX for controlling expression of endoplasmic reticulum chaperone, useful
XX for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX capable of regulating transcription inducing activity exhibited by an
XX element (ERSE) can be used in a method for controlling expression of
XX an endoplasmic reticulum chaperone. The method comprises expressing
XX bZIP. The method can be used for expression of a foreign protein by
XX positively regulating expression of an endoplasmic reticulum
XX chaperone gene. bZIP is useful for controlling the expression of
XX endoplasmic reticulum chaperone either positively or negatively in
XX cells and therefore is useful for treatment or prophylaxis of
XX cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
XX wounds and ulcers. bZIP also maintains the correct conformation of
XX the endoplasmic reticulum chaperone and thereby increases the
XX expression of a foreign protein. This sequence taken from the
XX glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
XX sequence.
XX
XX Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other:
SQ
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1,4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATGCAGCGCCGACG 19
RESULT 18
AAA28577
ID AAA28577 standard; DNA; 19 BP.
XX
XX AAA28577;
XX
XX 29-AUG-2000 (first entry)
XX
XX Calreticulin promoter ERSE3-like sequence.
XX
XX Endoplasmic reticulum stress; ER; transcription factor;
XX transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
XX cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
XX gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Homo sapiens.
XX
XX WO200029429-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-JP06305.
XX
XX 13-NOV-1998; 98JP-0324227.
XX
XX 13-NOV-1998; 98JP-0324227.

PR 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI: 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX for controlling expression of endoplasmic reticulum chaperone, useful
XX for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX capable of regulating transcription inducing activity exhibited by an
XX element (ERSE) can be used in a method for controlling expression of
XX an endoplasmic reticulum chaperone. The method comprises expressing
XX bZIP. The method can be used for expression of a foreign protein by
XX positively regulating expression of an endoplasmic reticulum
XX chaperone gene. bZIP is useful for controlling the expression of
XX endoplasmic reticulum chaperone either positively or negatively in
XX cells and therefore is useful for treatment or prophylaxis of
XX cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
XX wounds and ulcers. bZIP also maintains the correct conformation of
XX the endoplasmic reticulum chaperone and thereby increases the
XX expression of a foreign protein. This sequence taken from the
XX calreticulin (CRT) promoter contains an ERSE like sequence.
XX
XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other:
SQ
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1,4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATGCAGCGCCGACG 19
RESULT 19
AAA28578
ID AAA28578 standard; DNA; 19 BP.
XX
XX AAA28578;
XX
XX 29-AUG-2000 (first entry)
XX
XX Calreticulin promoter ERSE3-like sequence.
XX
XX Endoplasmic reticulum stress; ER; transcription factor;
XX transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
XX cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
XX gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX Mus musculus.
XX
XX WO200029429-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-JP06305.
XX
XX 13-NOV-1998; 98JP-0324227.
XX
XX 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX WPI: 2000-387736/33.

XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
PS Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC calreticulin (CRT) promoter contains an ERSE like sequence.
CC
SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATGAGGTCGACCACG 19
RESULT 20
AAA28680
ID AAA28680 standard; DNA: 19 BP.
XX
AC AAA28680;
XX
DT 29-AUG-2000 (first entry)
XX
DE ERSE1 consensus sequence.
XX
KW Endoplasmic reticulum stress; ER: transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene;
KW gene expression; GRP; glucose regulated protein; promoter; ss.
XX
OS Synthetic.
XX
PN WO200029429-A2.
XX
PD 25-MAY-2000.
XX
PE 12-NOV-1999; 99WO-JP06305.
XX
PR 13-NOV-1998; 98JP-0324227.
XX
PR 09-JUN-1999; 99JP-0163112.
XX
PA (HSPR-) HSP RES INST INC.
XX
PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
DR WPI; 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
PS Claim 1; Page 130; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of a foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of
CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein.
CC
SQ Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 100.0%; Pred No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATNNNNNNNNCCACG 19
RESULT 21
AAI70001
ID AAI70001 standard; DNA: 19 BP.
XX
AC AAI70001;
XX
DT 19-DIC-2001 (first entry)
XX
DE ERSE consensus sequence.
XX
KW ORP150; drug; ischemic disease; wound; ulcer; diabetes; ERSE;
KW neurodegenerative disease; cancer; autoimmune disease; promoter; ds.
XX
OS Unidentified.
XX
OS JP2001238699-A.
XX
PN 04-SEP-2001.
XX
PD 01-MAR-2000; 2000JP-0055384.
XX
PR 01-MAR-2000; 2000JP-0055384.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
DR WPI; 2001-610059/70.
XX
PT Screening a substance for controlling ORP150 expression, used for
PT produce drugs for the treatment of diseases associated with ORP150
PT expression -
XX
PS Example 3; Page 9; 9pp; Japanese.
XX
XX The present invention relates to a method for screening a substance for
CC controlling ORP150 expression. The method comprises examining the
CC expression of a reporter gene product in the presence of a cell strain
CC transformed by a vector. In the vector, the reporter gene is connected
CC downstream of the promoter region of ORP150 gene and a sample to be
CC tested. The method can be used to obtain drug compositions which alter
CC ORP150 expression. The drug composition can be used for the treatment of
CC various diseases e.g. ischemic diseases, wounds, ulcers, diabetes,
CC neurodegenerative diseases, cancers or autoimmune diseases. The present
CC sequence is an ERSE consensus sequence which was used in an example from
CC the present invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match
 Best Local Similarity 52.6%; Score 10; DB 22; Length 19;
 Matches 19; Conservative 100.0%; Pred. No. 1.4e+03;
 Mismatches 0; Indels 0; Gaps 0;
 Db 1 CCAATNNNNNNNNCCACG 19
 1 CCAATNNNNNNNNCCACG 19

RESULT 22

AA28780
 ID AAF28780 standard; DNA; 19 BP.

AC AAF28780;

DT 09-APR-2001 (first entry)

DE Endoplasmic response stress element motif.

KW Cytostatic; antidiabetic; dermatological; hepatotropic; gene therapy;
 KW heterologous gene expression; stress-responsive regulatory sequence;
 KW endoplasmic reticulum stress element; ERSE; glucose responsive protein;
 KW gpr78; promoter; cell proliferative disorder; inflammation; cancer;
 KW diabetes; human; transgenic animal; ss.

OS Unidentified.

FT Key Location/Qualifiers
 FT protein_bind 1..5

FT misc_feature /tag= a
 FT /bound_moiety= "CBF/NF- γ proteins"

FT /tag= b
 FT /note= "GC-rich region"

FT protein_bind 15..19
 FT /tag= c
 FT /bound_moiety= "Y1 protein"

PN MO200100791-A1.

PD 04-JAN-2001.

PF 28-JUN-2000; 2000WO-US17885.

PR 28-JUN-1999; 99US-0141505.

PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

PI Lee AS;

DR WPI; 2001-071484/08.

PT A nucleic acid construct comprises a stress-responsive non-coding
 PT regulatory sequence useful in treating and detecting cell proliferative
 PT disorders, e.g. cancer, or biological stress resulting from glucose
 PT starvation, e.g. diabetes -

PS Claim 1; Page 83; 121pp; English.

CC Targeted gene expression is tool used for gene therapy of diseases and
 CC is based on 2 main strategies: (1) targeted entry of a heterologous
 CC nucleic acid to a host cell; and (2) specific tissue or cell expression
 CC of the heterologous gene. In general, heterologous gene expression has
 CC been controlled in transformed mammalian cells by the constitutive
 CC promoter purpose Murine Leukemia Virus (MLV) Long Terminal Repeat (LTR)
 CC expresses the heterologous gene in a biologically stressed environment.
 CC The current invention thus relates to a nucleic acid construct comprising
 CC at least one stress-responsive non-coding regulatory sequence comprising
 CC at least two copies of an endoplasmic reticulum stress element (ERSE).
 CC The preferred ERSE of the invention is the sequence shown here which
 CC corresponds to a glucose responsive protein (grp) 78 gene promoter ERSE.
 CC The construct also comprises a heterologous nucleic acid sequence

CC operatively linked to the regulatory sequence, where expression of the
 CC heterologous sequence is regulated by the non-coding sequence and where
 CC the heterologous sequence encodes a therapeutic agent effective for
 CC treating a cell proliferative disorder or for treating a disorder
 CC associated with glucose starvation or a detectable marker. The invention
 CC is useful for treating or detecting a cell proliferative disorder
 CC possibly associated with inflammation, for example neoplastic disorder
 CC such as lung cancer, colon-rectum cancer, breast cancer, prostate cancer,
 CC urinary tract cancer, leukemia, melanoma, stomach cancer, pancreatic
 CC cancer, leukemia, melanoma, stomach cancer, thyroid cancer, liver cancer,
 CC brain cancer and ovarian cancer. The invention is also useful for
 CC treating a disorder associated with glucose starvation, such as diabetes.
 CC Non-human transgenic animals of the invention include vertebrates such
 CC as rodents, non-human primates, sheep, dogs, cows, pigs, amphibians, and
 CC reptiles.

SQ Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match
 Best Local Similarity 52.6%; Score 10; DB 22; Length 19;
 Matches 19; Conservative 100.0%; Pred. No. 1.4e+03;
 Mismatches 0; Indels 0; Gaps 0;

Db 1 CCAATNNNNNNNNCCACG 19
 1 CCAATNNNNNNNNCCACG 19

RESULT 23
 AAA28596
 ID AAA28596 standard; DNA; 24 BP.

AC AAA28596;

DT 29-AUG-2000 (first entry)

DE GRP78 promoter ERSE1-like sequence.

XX

KW Endoplasmic reticulum stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW cystic fibrosis; cancer; arteriosclerosis; ischemia; wound healing;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.

OS Unspecified.

PN WO200029429-A2.

PD 25-MAY-2000.

PF 12-NOV-1999; 99WO-JP06305.

PR 13-NOV-1998; 98JP-0324227.

PR 09-JUN-1999; 99JP-0163112.

PA (HSPR-) HSP RES INST INC.

PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

DR WPI; 2000-387736/33.

PT New endoplasmic reticulum stress transcription factor (known as bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers

PS Example 1; Fig 7; 157pp; English.

CC An endoplasmic reticulum stress transcription factor (bZIP)
 CC capable of regulating transcription inducing activity exhibited by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum

XX OS Synthetic.
XX PN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 144; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,
XX CC which further comprises detecting the presence of the modified target
XX CC nucleic acid.
XX SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 52.6%; Score 10; DB 24; Length 24;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 CCAATNNNNNNNNCCAG 19
XX 11111
XX 2 CCAATATTACGTGACCACG 20
XX
XX RESULT 27
XX ID ABQ10685/C
XX ABQ10685 standard; DNA; 24 BP.
XX AC ABQ10685;
XX DT 11-JUN-2002 (first entry)
XX DE Oligonucleotide adapter/capture probe 10676.
XX KM Oligonucleotide array; adapter sequence; probe; ss.
XX OS Synthetic.
XX OS WO200216649-A2.
XX FN 28-FEB-2002.
XX PD 27-AUG-2001; 2001WO-US26519.
XX PF 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX

DR WPI; 2002-292068/33.
XX
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 221; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,
XX CC which further comprises detecting the presence of the modified target
XX CC nucleic acid.
XX SQ Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 52.6%; Score 10; DB 24; Length 24;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 CCAATNNNNNNNNCCAG 19
XX 11111
XX 23 CCAATATTACGTGACCACG 5
XX
XX Db
XX
XX RESULT 28
XX ID ABQ10726
XX ABQ10726 standard; DNA; 24 BP.
XX AC ABQ10726;
XX DT 11-JUN-2002 (first entry)
XX DE Oligonucleotide adapter/capture probe 10717.
XX KM Oligonucleotide array; adapter sequence; probe; ss.
XX OS Synthetic.
XX OS WO200216649-A2.
XX FN 28-FEB-2002.
XX PD 27-AUG-2001; 2001WO-US26519.
XX PF 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 221; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,

CC which further comprises detecting the presence of the modified target nucleic acid.

XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

XX Query Match 52.6%; Score 10; DB 24; Length 24;

XX Best Local Similarity 52.6%; Pred. No. 1.5e+03;

XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19

DB 2 CCAATATTACGTGACCCAG 20

RESULT 29

AAV45529/C

ID AAV45529 standard; DNA; 25 BP.

XX AAV45529;

XX 15-FEB-1999 (first entry)

XX Helicobacter pylori ureg gene PCR primer.

XX Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;

XX stomach cancer; ureg gene; PCR; primer; ss.

XX Synthetic.

XX Helicobacter pylori.

XX WO9844130-A1.

XX 08-OCT-1998.

XX 31-MAR-1998; 98WO-KR00073.

XX 31-MAR-1997; 97KR-0011951.

XX 31-MAR-1997; 97KR-0011950.

XX (DAEW-) DAEWONG PHARM CO LTD.

XX Choi D, Jung H, Kim B, Park M, Shin S, Yu Y;

XX WPI; 1998-568279/48.

XX New chimeric proteins for use against Helicobacter pylori

XX comprising an antigenic protein of H. pylori and A1 and B subunits

XX of Vibrio cholerae toxin, preferably produced by recombinant

XX techniques

XX Example 2-15; Page 13; 102pp; English.

XX PCR primers (see AAV45529 and AAV45530) are designed for the PCR

XX amplification of the Helicobacter pylori ureg gene. The invention

XX relates to recombinant DNA (see AAV62460-61) comprising a fusion gene

XX prepared by ligating an antigenic determinant coding gene (e.g. the

XX ureg gene) of H. pylori and A2 and B subunit genes of Vibrio

XX cholerae. Also claimed are chimeric proteins (see AAW60599-600)

XX encoded by such recombinant DNAs, methods for the recombinant

XX production of the chimeric proteins, and use of the chimeric

XX proteins in preventative and therapeutic vaccines for H. pylori-

XX associated diseases such as gastritis, gastric ulcer, duodenal

XX ulcer and gastric cancer.

XX Sequence 25 BP; 7 A; 2 C; 8 G; 8 T; 0 other;

XX Query Match 52.6%; Score 10; DB 19; Length 25;

XX Best Local Similarity 52.6%; Pred. No. 1.5e+03;

XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19

DB 20 CCAATTTTACGTGACCCAG 2

RESULT 30

AB012221/C

ID AB012221 standard; DNA; 25 BP.

XX AB012221;

XX 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 12212.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting

XX a target nucleic acid sequence, has different addresses comprising

XX different specific capture probes

XX Claim 1; Page 240; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least

XX 25 different addresses (adapter sequences) with each comprising a

XX different capture probe selected from a group consisting of the sequences

XX given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target

XX nucleic acid sequence by attaching an adapter nucleic acid

XX (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target

XX nucleic acid and contacting the modified target nucleic acid with (I).

XX The steps of above method is useful for detecting a target nucleic acid,

XX which further comprises detecting the presence of the modified target

XX nucleic acid.

XX Sequence 25 BP; 4 A; 5 C; 9 G; 7 T; 0 other;

XX Query Match 52.6%; Score 10; DB 24; Length 25;

XX Best Local Similarity 52.6%; Pred. No. 1.5e+03;

XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19

DB 24 CCAATATTACGTGACCCAG 6

Search completed: November 16, 2002, 02:15:58
Job time : 260 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:09:22 ; Search time 1972 Seconds
(without alignments)
156.042 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19
Sequence: 1 ccaatnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estp1:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	43	17	BH857113
2	10	52.6	76	9	AA475936
3	10	52.6	79	14	B0756881
4	10	52.6	80	17	BH251489
5	10	52.6	82	14	B0099298
6	10	52.6	86	17	BH232183

C 7	10	52.6	97	17	BH222106	BH222106 1006105C1
C 8	10	52.6	99	17	AZ921866	AZ921866 HRCOT4D10
C 9	10	52.6	100	12	BF086094	BF086094 CM3-GN005
C 10	10	52.6	101	17	BH583741	BH583741 BOGXN16TR
C 11	10	52.6	103	9	AA927925	AA927925 OM23B01.5
C 12	10	52.6	109	17	BH864991	BH864991 SALK_0972
C 13	10	52.6	110	12	BF094257	BF094257 CM4-UT004
C 14	10	52.6	110	17	AZ720239	AZ720239 RPCI-24-1
C 15	10	52.6	113	17	BH222899	BH222899 1006109HO
C 16	10	52.6	115	9	A1938545	A1938545 SB5502.Y
C 17	10	52.6	115	10	AW945325	AW945325 PM3-EN000
C 18	10	52.6	115	13	BG950375	BG950375 CM3-CT060
C 19	10	52.6	115	17	AG024826	AG024826 Oryza sat
C 20	10	52.6	119	9	A1549504	A1549504 UI-R-C3-L
C 21	10	52.6	120	17	BH230343	BH230343 1006157D1
C 22	10	52.6	121	17	BH222096	BH222096 1006105C0
C 23	10	52.6	123	9	AA405167	AA405167 zUS1H01.r
C 24	10	52.6	124	17	AQ073902	AQ073902 EP(3)3309
C 25	10	52.6	124	17	BH812753	BH812753 SALK_0630
C 26	10	52.6	124	17	BH847929	BH847929 SALK_0660
C 27	10	52.6	129	17	AZ919927	AZ919927 1006017C0
C 28	10	52.6	130	17	BH895687	BH895687 3526.1.35
C 29	10	52.6	132	12	BE936064	BE936064 QV2-NN005
C 30	10	52.6	132	12	BF361951	BF361951 QV2-NN004
C 31	10	52.6	132	17	BH753521	BH753521 SALK_0292
C 32	10	52.6	132	17	BH854781	BH854781 SALK_0886
C 33	10	52.6	133	17	AZ726948	AZ726948 RPCI-24-1
C 34	10	52.6	135	10	AV963893	AV963893 AV963893
C 35	10	52.6	137	9	AA168302	AA168302 mS54a10.r
C 36	10	52.6	137	13	BM645289	BM645289 170006873
C 37	10	52.6	138	10	BE002165	BE002165 PM2-BN008
C 38	10	52.6	140	9	AV060848	AV060848 AV060848
C 39	10	52.6	141	10	AV957023	AV957023 AV957023
C 40	10	52.6	143	10	AV388329	AV388329 AV388329
C 41	10	52.6	145	9	A1843915	A1843915 UI-M-AP1
C 42	10	52.6	145	10	BE151291	BE151291 CM1-HT028
C 43	10	52.6	146	10	AM449763	AM449763 UI-H-B13
C 44	10	52.6	146	12	BG411131	BG411131 602498760
C 45	10	52.6	148	10	AM121751	AM121751 UI-M-BH2
C 46	10	52.6	148	10	BE151588	BE151588 UI-R-B11
C 47	10	52.6	149	10	BB606552	BB606552 BB606552
C 48	10	52.6	149	17	BH229683	BH229683 100615360
C 49	10	52.6	150	17	AZ973950	AZ973950 2M0248823
C 50	10	52.6	152	17	BH197483	BH197483 TC3-59E3
C 51	10	52.6	152	17	BH790242	BH790242 SALK_0566
C 52	10	52.6	155	9	AV010555	AV010555 AV010555
C 53	10	52.6	155	10	AW371361	AW371361 RC0-BT028
C 54	10	52.6	156	10	AM091112	AM091112 614090E11
C 55	10	52.6	156	10	BB786641	BB786641 BB786641
C 56	10	52.6	157	9	A1817561	A1817561 WK24G07.X
C 57	10	52.6	158	9	A1964826	A1964826 ZF-EST327
C 58	10	52.6	158	12	BE712044	BE712044 QV2-HT069
C 59	10	52.6	159	9	AJ237134	AJ237134 AJ237134
C 60	10	52.6	159	9	AV289314	AV289314 AV289314
C 61	10	52.6	159	13	BI399749	BI399749 M1-P-AV1
C 62	10	52.6	159	13	BI406859	BI406859 182D02.Ma
C 63	10	52.6	161	13	BI059548	BI059548 IL3-HT011
C 64	10	52.6	163	13	BI742019	BI742019 Kt84G06.Y
C 65	10	52.6	164	13	BI023913	BI023913 MR3-MT032
C 66	10	52.6	165	12	BG090373	BG090373 mac19H08
C 67	10	52.6	167	12	BF749006	BF749006 MR2-BN038
C 68	10	52.6	167	10	BB001165	BB001165 BB001165
C 69	10	52.6	168	9	AA749830	AA749830 ISAS0335
C 70	10	52.6	168	9	A1846641	A1846641 UI-M-NT1
C 71	10	52.6	168	10	BE087363	BE087363 QV1-BT068
C 72	10	52.6	169	13	BI088613	BI088613 602853166
C 73	10	52.6	170	12	BF733308	BF733308 MR0-AN003
C 74	10	52.6	170	13	BI799942	BI799942 H144C07.E
C 75	10	52.6	171	13	BI047605	BI047605 MR4-ST024
C 76	10	52.6	172	9	AV060234	AV060234 AV060234
C 77	10	52.6	172	9	AV086215	AV086215 AV086215
C 78	10	52.6	172	13	BM195701	BM195701 C0315A05-
C 79	10	52.6	173	9	AA684809	AA684809 EST105472

C	80	10	52.6	173	12	BF748094	BF748094	MR2-BN038
	81	10	52.6	173	12	BH789270	BH789270	SALK_0014
C	82	10	52.6	174	9	AV004354	AV004354	AV004354
	83	10	52.6	174	13	B1J21753	B1J21753	B1J21753
	84	10	52.6	174	17	BH895513	BH895513	3526_1_34
C	85	10	52.6	175	9	AV022317	AV022317	AV022317
	86	10	52.6	175	9	AA556235	AA556235	vo30110_r
	87	10	52.6	175	17	BH855839	BH855839	SALK_0844
	88	10	52.6	176	12	BF347368	BF347368	60202056
	89	10	52.6	178	9	A1937584	A1937584	WP81C04_x
C	90	10	52.6	178	9	AV097435	AV097435	AV097435

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
BH857113	43 bp	DNA linear GSS 08-JUL-2002
BH857113		SAIK_076821.44.95.x Arabidopsis thaliana TMA insertion lines

ACCESSION	BH857113
VERSION	BH857113.1
KEYWORDS	GSS.
SOURCE	thale cress.

REFERENCE	1 (bases 1 to 43)
AUTHORS	Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab

TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker

JOURNAL COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Laboratories (SIGLAB)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeresalk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g29100.
Class: TDNA tagged.

FEATURES	Location/Qualifiers
source	1. .43

```

/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_id="SALK_076821.44.95.X"
/clone_id="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

```

Query Match	52.6%	Score 10:	DB 17:	Length 43:
Best Local Similarity	52.6%	Pred. No.	1.5e+04:	
Matches 10:	Conservative	0:	Mismatches 9:	Indels 0:
				Gaps 0:

QY 1 CCAATNNNNNNNNNNCCACG 19
11111 11111
Db 18 CCAATGAATTACGCCACG 36

RESULT 2

AA475936					
LOCUS	AA475936	76 bp	mRNA	linear	EST 18-JUN-1997
DEFINITION	vh25b10.r1 Soares_mammary_gland_NbMxg Mus musculus				CDNA clone

ACCESSION	AA475936
VERSION	AA475936.1
KEYWORDS	GI:2203787
SOURCE	EST.
ORGANISM	house mouse, Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project

WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
Trace considered overall poor quality
Possible reversed clone: similarly on wrong strand
Seq primer: -28m13 rev2 EF from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .76
SOURCE

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone IMAGE:876475"
/clone_lib="Soares_mammary_gland_NbMNG"
/sex="male"
/tissue_type="mammary_gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Fac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',

```

BASE COUNT
ORIGIN

19 a 28 c 16 g 13 t

TTTTCACATCTGTAAGATGGGAGCGCGCGCAATAGCTTTTTTTTTTTTTTTTTTTT
T 3 1; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

Query Match	52.6%	Score 10;	DB 9;	Length 76;
Best Local Similarity	52.6%	Pred. No. 1.9e+04;		
Matches 10;	Conservative	0;	Mismatches 9;	Indels 0;
QY	1	CCAATTNNNNNNNNCCACG	19	
Db	40	CCAATGGTTTAGCGCCACG	58	

RESULT 3	
BQ756881	
LOCUS	79 bp mRNA linear EST 26-JUL-2002
DEFINITION	BQ756881 Ebm005.SG0005.E15.R embryo, 1 Day germination, no treatment, cv Ebm005, Ebm009 Hordeum vulgare cDNA clone Ebm005.SG005.E15 5', mRNA

Sequence.
 ACCESSION B0756881 GI:21965353
 VERSION B0756881.1
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae

REFERENCE 1 (bases 1 to 79)
 Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 Development of barley transcriptome resources
 Unpublished (2001)
 Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: estescr@sari.ac.uk.

FEATURES
 source Location/Qualifiers
 1..79
 /organism="Hordeum vulgare"
 /cultivar="Optic"
 /db_xref="taxon:4513"
 /clone="EBem09_SQ005_E15"
 /clone_lib="Embryo, 1 Day germination, no treatment, cv
 Optic, EBem09"
 /issue_type="embryo"
 /dev_stage="1 Day germination"
 /lab_host="DH10B"
 /note="Vector: pSPORT1. Site_1: Sal I; Site_2: Not I.
 Non-normalised library; directionally cloned into pSPORT1.
 Derived from embryos dissected from germinating grains (1
 day) in glasshouse grown barley plants. Developed as part
 of the barley transcriptome resources of BBSRC/SERAD
 funded cereal IGP (Investigating Gene Function) project."

BASE COUNT 19 a 18 c 17 g 25 t

ORIGIN

Query Match 52.6%; Score 10; DB 14; Length 79;
 Best Local Similarity 52.6%; Pred. No. 1.9e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 42 CCAATTTGTCACACG 60

RESULT 4 80 bp DNA linear GSS 28-NOV-2001
 BH251489/c
 LOCUS SALK_011672 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 DEFINITION thaliana genomic clone SALK_011672, DNA sequence.
 ACCESSION BH251489
 VERSION BH251489.1 GI:17138467
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 80)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab,
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies

JOURNAL
 COMMENT

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckersalk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..80
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_011672"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 18 a 20 c 21 g 19 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 80;
 Best Local Similarity 52.6%; Pred. No. 1.9e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 26 CCAATGATAAATAGCCACG 8

RESULT 5 82 bp mRNA linear EST 10-APR-2002
 BQ099298
 LOCUS pn28h02.y2 Ostertagia ostertagi L3 PAMPI v1 Ostertagia ostertagi
 DEFINITION cDNA 5', mRNA sequence.
 ACCESSION BQ099298
 VERSION BQ099298.1 GI:20132282
 KEYWORDS EST.
 SOURCE Ostertagia ostertagi.
 ORGANISM Ostertagia ostertagi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Strongylida;
 Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
 1 (bases 1 to 82)
 McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wylie, T.,
 Dante, M., Mairra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
 Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarelis, V., R.,
 Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
 M., Allen, M., Person, B., Swaller, T., Harvey, N., Schuck, R., Kohn, S.,
 Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
 Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High quality sequence stop: 69.
 Location/Qualifiers
 1..82
 /organism="Ostertagia ostertagi"
 /db_xref="taxon:6317"
 /clone_lib="Ostertagia ostertagi L3 PAMPI v1"
 /dev_stage="L3"
 /lab_host="DH10B"
 /note="Vector: PAMPI (Gibco); Site_1: NotI; Site_2: SalI;

JOURNAL
 COMMENT

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgsbarre@nrl.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of *Osteria* eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

BASE COUNT 24 a 24 c 12 g 22 t
ORIGIN

Query Match 52.6%; Score 10; DB 14; Length 82;
Best Local Similarity 52.6%; Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 12 CCAATGAGAGTGTCCAGC 30

RESULT 6
BH232183/c 86 bp DNA linear GSS 08-NOV-2001
LOCUS 1006166D12.y1 1006 - Rescemu Grid G Zea mays genomic, DNA
DEFINITION
sequence.
ACCESSION BH232183
VERSION BH232183.1 GI:16837119
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 86)

REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered Rescemu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006166 row: 23
Class: transposon-tagged.

FEATURES

source
Location/Qualifiers
1..86
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was

extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 13 a 24 c 37 g 12 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 86;
Best Local Similarity 52.6%; Pred. No. 2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 61 CCAATCATGTGAGCCAGC 43

RESULT 7
BH222106/c 97 bp DNA linear GSS 08-NOV-2001
LOCUS 1006105C10.x1 1006 - Rescemu Grid G Zea mays genomic, DNA
DEFINITION
sequence.
ACCESSION BH222106
VERSION BH222106.1 GI:16816606
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 97)

REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered Rescemu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 1006105 row: 13
Class: transposon-tagged.

FEATURES

source
Location/Qualifiers
1..97
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 27 c 44 g 15 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 97;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19

Db 92 CCAATTCGAGCACCACG 74

RESULT 8 A2921866 99 bp DNA linear GSS 07-JUN-2002

LOCUS A2921866 Sorghum bicolor HRCot Sorghum bicolor genomic, DNA

DEFINITION HRCotAD10

ACCESSION A2921866

VERSION A2921866.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Peterson DG
Plant Genome Mapping Laboratory
University of Georgia
Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA
30602, USA
Tel: 706-583-0167
Fax: 706-583-0160
Email: hydroxyapatite.fractionated DNA.
Class: Hydroxyapatite-fractionated DNA.

FEATURES

source

1. 99
Location/Qualifiers
/organism="Sorghum bicolor"
/cultivar="BTK623"
/db_xref="taxon:4558"
/clone_lib="Sorghum bicolor HRCot"
/issue_type="leaves"
/dev_stage="seedling"
/note="Vector: pGEM-TA-Easy; A Cot analysis was performed for the sorghum genome. Based on the resulting Cot curve, hydroxyapatite chromatography was used to isolate highly-repetitive (HR), moderately-repetitive (MR), and 'single/low-copy' (SL) sequence components from sheared genomic DNA. The three repetition-based DNA components were cloned into E. coli to produce HRCot, HRCot, and SLcot genomic libraries. Blotting and sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI Nr database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."

BASE COUNT

ORIGIN

18 a 19 c 29 g 33 t
Query Match 52.6%; Score 10; DB 17; Length 99;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY

Db

1 CCAATNNNNNNNNCCAG 19

56 CCAATTCGATTCGCCAG 38

RESULT 9

LOCUS

DEFINITION

BF086094 100 bp mRNA linear EST 19-OCT-2000
BF086094
CM3-GN0052-080900-334-cl1 GN0052 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF086094
VERSION BF086094.1
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=62=CM3-GN0052-080900-334-cl1&ts=2000-09-08&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 100.
Location/Qualifiers
1. 100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0052"
/dev_stage="adult"
/note="Organ: placenta normal; Vector: puc18; Site: 1; Smal
; Site: 2; Smal; A mini-library was made by cloning
products derived from ORSPRES PCR (U.S. Letters Patent
application No. 196,776 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

FEATURES

source

BASE COUNT 35 a 23 c 18 g 24 t
ORIGIN
Query Match 52.6%; Score 10; DB 12; Length 100;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY

Db

1 CCAATNNNNNNNNCCAG 19

82 CCAATTCGATTCGCCAG 100

RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF583741 101 bp DNA linear GSS 15-DEC-2001
BF583741
BOGXN16R BOGX Brassica oleracea genomic clone BOGXN16, DNA
sequence.
BF583741
BF583741.1 GI:17836198
GSS.
Brassica oleracea.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 101)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.

TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source location/Qualifiers

1..101
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone.lib="BOGXN16"
/note="Vector: PHOS1, site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 38 a 23 c 22 g 18 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 101;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 25 CCAATGCGGCGCCACG 43

RESULT 11
AA927925/c 103 bp mRNA linear EST 10-JUN-1998
LOCUS
DEFINITION om23b01.s1 Soares_NFL.T.GBC_SI Homo sapiens CDNA clone
IMAGE:1541833 3', mRNA sequence.
ACCESSION AA927925
VERSION AA927925.1 GI:3076669
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Tumor Gene Index

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 57.
location/Qualifiers

1..103
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="IMAGE:1541833"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p777D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP CCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNA from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239.

726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.
BASE COUNT 25 a 23 c 25 g 30 t
ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 103;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 55 CCAATTCATCGACACG 37

RESULT 12
BH864991/c 109 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_097225 Arabidopsis thaliana TDNA insertion lines
ACCESSION BH864991
VERSION BH864991.1 GI:22100889
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 109)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
location/Qualifiers

1..109
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone.lib="SALK_097225"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna-protocols.html"
BASE COUNT 22 a 29 c 24 g 34 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 109;
Best Local Similarity 52.6%; Pred. No. 2.2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 30 CCAATGTAAGACGACG 12

RESULT 13
BF094257
LOCUS
DEFINITION BF094257 110 bp mRNA linear EST 19-OCT-2000
CM4-UT0042-050900-568-e11 UT0042 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF094257
 VERSION BF094257.1 GI:10899967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 110)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. P., Goldman, G. H., Carvalho, A. F., Matsushima, A., Baia, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. O., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=at2-CM4-UT0042-050>)
 900-568-61163=2000-09-0564-1)
 Seq primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 109.
 Location/Qualifiers
 1..110
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UT0042"
 /dev_stage="Adult"
 /note="Organ: uterus; tumor; Vector: puc18; Site: 1; Smal; Site: 2; Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 26 a 38 c 23 g 23 t
 ORIGIN

Query Match 52.6%; Score 10; DB 12; Length 110;
 Best Local Similarity 52.6%; Pred. No. 2.2e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 5 CCAATCCCTTACTCCACG 23

RESULT 14
 A2720239 110 bp DNA linear GSS 24-JAN-2001
 LOCUS A2720239
 DEFINITION RPCI-24-104K1.TV RPCI-24 Mus musculus genomic clone RPCI-24-104K1,
 DNA sequence.
 VERSION A2720239
 KEYWORDS A2720239.1 GI:12461733
 SOURCE GSS
 ORGANISM house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 110)
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akimov, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,

TITLE Russell, D., de Jong, P. and Fraser, C.M.
 JOURNAL Mouse BAC End Sequences from Library RPCI-24
 COMMENT Unpublished (1999)
 Other GSS: RPCI-24-104K1.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
 Plate: 104 row: K column: 1
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..110
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-104K1"
 /clone_lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pPARBAC1; Site: 1: BamHI; Site: 2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pPARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 28 a 28 c 15 g 39 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 110;
 Best Local Similarity 52.6%; Pred. No. 2.2e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 52 CCAATCTTTCATCCACG 70

RESULT 15
 BH222899/c 113 bp DNA linear GSS 08-NOV-2001
 LOCUS BH222899
 DEFINITION 1006109H01.x1 1006 - Rescuemu Grid G zea mays genomic, DNA
 sequence.
 ACCESSION BH222899
 VERSION BH222899.1 GI:16818250
 KEYWORDS GSS.
 SOURCE Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 113)
 Walbot, V.
 Maize genomic sequences found using engineered Rescuemu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site so sequence was trimmed. Post-ligation
 sequence submitted separately.
 Plate: 1006109 row: 15
 Class: transposon-tagged.

BASE COUNT	37 a	21 c	25 g	32 t
ORIGIN	/clone.lib="EN0004" /dev_strage="Adult" /note="Organ: lung_normal; Vector: puc18; Site.1: Sma1; Site.2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,7716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
Query Match	52.6%;	Score 10;	DB 10;	Length 115;
Best Local Similarity	52.6%;	Pred. No. 2.2e+04;		
Matches	10;	Conservative	0;	Mismatches 9; Indels 0; Gaps 0;
QY	1	CCATNNNNNNNNCCAGC	19	
	11111	11111		
Db	83	CCAACTAAATATCCAGC	101	
RESULT 18				
LOCUS	BC950375	115 bp	mRNA	linear
DEFINITION	CM3-CT0603-040101-611-h01 CT0603 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	BC950375			
VERSION	BC950375.1	GI:14368546		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 115)			
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.			
	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
TITLE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
JOURNAL	2020263			
MEPLINE	Contact: Simpson A.J.G.			
COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CT0603 040101-611-h01&t3=2001-01-04&t4=1) Seq primer: puc 18 forward High quality sequence start: 22 High quality sequence stop: 115. Location/Qualifiers 1. 115 /organism="Homo sapiens" /db_xref="taxon:9606" /clone.lib="CT0603" /dev_strage="Adult" /note="Organ: colon; Vector: puc18; Site.1: Sma1; Site.2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 19 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
FEATURES				
source				
BASE COUNT	19 a	25 c	38 g	33 t
ORIGIN				

Query Match	52.6%	Score 10:	DB 13:	Length 115:
Best Local Similarity	52.6%	Pred. No. 2.2e+04:		
Matches 10: Conservative	0:	Mismatches 9:	Indels 0:	Gaps 0:
RESULT 19				
LOCUS AG024826				
DEFINITION	Oryza sativa (japonica cultivar-group) DNA, clone: T028697, 3 flanking sequence of Tos17 insertion in rice strain NC0370, genomic survey sequence.			
ACCESSION	AG024826			
VERSION	AG024826.1			
SOURCE	GSJ.			
ORGANISM	Oryza sativa (japonica cultivar-group) (strain: NC0370, cultivar: Nipponbare) DNA, clone: lib:PCR product directly amplified from rice genomic DNA clone: T028697.			
REFERENCE	Oryza sativa (japonica cultivar-group) (strain: NC0370, cultivar: Nipponbare) DNA, clone: lib:PCR product directly amplified from rice genomic DNA clone: T028697.			
AUTHORS	Myiyo, A., Miyazaki, A., Yamashita, Y. and Hirochika, H.			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
TITLE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
LOCUS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
DEFINITION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ACCESSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
VERSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
SOURCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ORGANISM	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
REFERENCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
TITLE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
LOCUS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
DEFINITION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
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VERSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
SOURCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ORGANISM	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
REFERENCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
TITLE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
LOCUS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
DEFINITION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ACCESSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
VERSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
SOURCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ORGANISM	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
REFERENCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
TITLE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
LOCUS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
DEFINITION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ACCESSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
VERSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
SOURCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ORGANISM	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
REFERENCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
TITLE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
AUTHORS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
JOURNAL	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
LOCUS	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
DEFINITION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ACCESSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
VERSION	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
SOURCE	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission			
ORGANISM	Submitted (25-OCT-1999) Akio Myiyo, National Institute of Direct Submission	</		

REFERENCE 1 (bases 1 to 119)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Seq primer: M13 forward.

FEATURES
 source
 1..119
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C3-tu-f-02-0-UI"
 /clone_1lb="UI-R-C3"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C3) was constructed as follows: PCR amplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)."

BASE COUNT 23 a 20 c 32 g 44 t
 ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 119;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
 ||||| |||||
 Db 119 CCAATGCTTACCTCCAGC 101

RESULT 21 120 bp DNA linear GSS 08-NOV-2001
 LOCUS BH230343/c
 DEFINITION 1006157D12.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
 ACCESSION BH230343
 VERSION BH230343.1 GI:16833394

KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 120)
 REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site found so sequence was trimmed.
 Post-ligation sequence submitted separately.
 Plate: 1006157 row: 13
 Class: transposon-tagged.

FEATURES
 source
 1..120
 Location/Qualifiers
 /organism="Zea mays"
 /cultivar="mixed background W23/A18/B73"
 /db_xref="taxon:4577"
 /clone_1lb="1006 - RescueMu Grid G"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: Leaf; Vector: RescueMu (engineered from Bluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 12 a 31 c 51 g 26 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 120;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
 ||||| |||||
 Db 91 CCAATTCAAGCACCACG 73

RESULT 22 121 bp DNA linear GSS 08-NOV-2001
 LOCUS BH222096/c
 DEFINITION 1006105C05.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
 ACCESSION BH222096
 VERSION BH222096.1 GI:16816585
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 121)
 REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotstanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006105 row: 13
Class: transposon-tagged.

FEATURES

Source

1. 121
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone). Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iasate.edu' and follow the links for
'RescueMu', 'Grid G' was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT

12 a 33 c 51 g 25 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 121;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 92 CCAATTCGACGCCACCAGC 74
|||||

RESULT 23 123 bp mRNA linear EST 17-MAY-1997
AA405167
LOCUS z51H01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:741553 5', mRNA sequence.

ACCESSION AA405167
VERSION AA405167.1 GI:2063527
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le-N., Lennon, G., Marra, M., Martin, J., Moore, B.,
'Schellenberg, R., Stieple, M., Tan, F., Theising, B., White, Y., Wylie,
'T., Waterston, R. and Wilson, R.
WashU-Merck EST project 1997
Unpublished (1997)

TITLE

JOURNAL
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: estewartson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.

FEATURES

1. 123
/organism="Homo sapiens"

/db_xref="GDB:5941690"
/db_xref="taxon:9606"
/clone="IMAGE:741553"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGACAGTGGGACGGCGGCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT

23 a 37 c 27 g 36 t

ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 123;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 4 CCAATTCGTCGCCACCAGC 22
|||||

RESULT 24 124 bp DNA linear GSS 23-AUG-2000
AA073902
LOCUS EP(3)3309-5prime Drosophila melanogaster EP line Drosophila
DEFINITION melanogaster genomic Sequence recovered from 5' end of P element,
DNA sequence.

ACCESSION AA073902
VERSION AA073902.1 GI:3403944
KEYWORDS GSS.
SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 124)
Liao, G.-C., Rehm, E.J. and Rubin, G.M.
Insertion site preferences of the P transposable element in
Drosophila melanogaster
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)

REFERENCE

AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 117 in the 124 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers

FEATURES

Source

1. 124
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
insertion strains is described in North P., Szabo K., Bailey
A., Laverly T., Rehm J., Rubin GM, Weigmann K, Milan M, Benes

V, Ansoorge W, Cohen SM. 1998. Systematic gain-of-function genetics in *Drosophila*. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/P-distrupt/Inverse_pcr.html.

Query Match	52.68;	Score 10;	DB 17;	Length 124;
Best Local Similarity	52.68;	Pred. No. 2.3e+04;		
Matches 10;	Conservative 0;	Mismatches 9;	Indels 0;	Score 0

QY	1	CCATNNNNNNNNCCACG	19
Db	85	CCATTATCATTTCCACG	103

RESULT 25	BH812753/c			
LOCUS	BH812753	124 bp	DNA	linear
DEFINITION	SAIK_063023 Arabidopsis thaliana TNA insertion lines Arabidopsis			
ACCESSION	thaliana genomic clone SAIK_063023, DNA sequence.			
	BH812753			

REFERENCE
1 (bases 1 to 124)
1 bases; Brassicaceae; Arabidopsis.

TITLE	A sequence-indexed library of insertion mutations in the <i>Arabidopsis</i> genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker

```
class: IDNA tagged.
```

29 a 13 c 39 g 43 t

1 CCAATNNNNNNNNNNCCACG 19
 |||||
 117 CCAATAGTTTATTTCACG 99

RESULT 26				
BH847929/c				
LOCUS				
DEFINITION	BH847929	124 bp	DNA	
	SALK_066091.36.55.x	Arabidopsis thaliana	TPDN insertion	linear
				GSS 13-JUN-2002

ACCESSION	BH847929
VERSION	BH847929.1
KEYWORDS	GI:2141800
SOURCE	GSS.
	thale cress.

C., Jeske, A., Karnes, M., Kucenas, P., Chen, H., Cheuk, R., Gadrinab
 A., Zimmerman, J., and Ecker, J. R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TNA.
Class: TNA tagged.

```

FEATURES
SOURCE
Location/Qualifiers
1. 124
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK-066091.36.55.x"
/clone_11b="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence
at the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
38 a 20 c 35 g 31 t

```

Query Match	52.6%	Score 10;	DB 17;	Length 124;
Best Local Similarity	52.6%	Pred. No. 2.3e+04;		
Matches 10; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;
1 CCAATTNNNNNNNNCCACG 19				
b 116 CCAATTACACATACGCCACG 98				

RESULT 27	2219927/c	129 bp	DNA	linear	GSS 17-Dec-2001
DEFINITION	1006017C09.x1	1006	-	RescueHu Grid G	Zea mays genomic, DNA
FEATURES	1006017C09.x1				
ORIGIN	1006017C09.x1				
REMARKS					

REFERENCES
 AUTHOR S
 TITLE
 Maize genomic sequences found using engineered *Bar* gene, transposon
 AZ9942/1 GI:13390126
 GSS.
 SOURCE
 ORGANISM
 Zea mays.
 Zea mays
 Embryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 129)
 Walbot,V.

JOURNAL
COMMENT

Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006017 row: 37
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1. 129

/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf. Vector: RescueMu (engineered from pBluescript backbone). Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

29 a 34 c 48 g 18 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 129;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
|||||

Db 101 CCAATCCCGCCGCCACG 83

RESULT 28

BH895687

LOCUS

3526.1.35.1-C06.2BL.X_1 3526 - RescueMu Grid K Zea mays genomic,
DNA sequence.

ACCESSION

BH895687

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3526.1.35.1 row: 27
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1. 130

/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="3526 - RescueMu Grid K"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf. Vector: RescueMu (engineered from pBluescript backbone). Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

20 a 63 c 29 g 18 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 130;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
|||||

Db 34 CCAATCCTGTGCGTCACG 52

RESULT 29

BE936064

LOCUS

OV2-NN0054-230800-333-g09 NN0054 Homo sapiens cDNA, mRNA sequence.
BE936064

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 132)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=612=OV2-NN0054-230800-333-g09&l3=2000-08-23&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 132.

FEATURES

source

Location/Qualifiers
1. 132
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

/clone_lib="NN0054"
/dev_stage="Adult"
/site="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      46 a      27 c      31 g      28 t
ORIGIN

```

```

Query Match      52.6%; Score 10; DB 12; Length 132;
Best Local Similarity 52.6%; Pred. No. 2.4e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY      1 CCAATNNNNNNNNCCACG 19
        |||||
Db      27 CCAATTGACACCTTCACG 45

```

```

RESULT 30
BF361951      132 bp      mRNA      linear      EST 24-NOV-2000
LOCUS      BF361951
DEFINITION      QV2-NN0042-210800-310-d07 NN0042 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BF361951
VERSION      BF361951.1 GI:11323976
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
              M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
              20202663
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&lt2=QV2-NN0042-
210800-310-d07&lt3=2000-08-21&lt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 132.

```

FEATURES

```

Location/Qualifiers
1..132

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/clone_lib="NN0042"
/dev_stage="Adult"

```

```

/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

```

BASE COUNT      40 a      37 c      29 g      26 t
ORIGIN

```

```

Query Match      52.6%; Score 10; DB 12; Length 132;
Best Local Similarity 52.6%; Pred. No. 2.4e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY      1 CCAATNNNNNNNNCCACG 19
        |||||
Db      46 CCAATTCCTGACACACACG 64

```

```

Search completed: November 16, 2002, 03:32:34
Job time : 1980 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:59:22 : Search time 47 Seconds
(without alignments)
149.377 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19 ccaatnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 328367 seqs, 184756068 residues

Total number of hits satisfying chosen parameters: 656734

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCRTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/PCRTUS_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.6	25	10	US-09-402-100-35	Sequence 35, App1
2	52.6	100	10	US-09-969-373-1152	Sequence 1152, Ap
3	52.6	123	10	US-09-867-701-3962	Sequence 3962, Ap
4	52.6	210	10	US-09-974-300-8096	Sequence 8096, Ap
5	52.6	214	10	US-09-778-320-59	Sequence 59, App1
6	52.6	214	10	US-09-910-689-59	Sequence 59, App1
7	52.6	214	12	US-10-010-742-59	Sequence 59, App1
8	52.6	219	10	US-09-783-590-10136	Sequence 10136, A
9	52.6	237	10	US-09-777-564-1013	Sequence 1013, Ap
10	52.6	238	10	US-09-960-352-13155	Sequence 13155, A
11	52.6	247	10	US-09-878-574-6181	Sequence 6181, Ap
12	52.6	261	10	US-09-604-287A-206	Sequence 206, App
13	52.6	261	10	US-09-339-338-206	Sequence 206, App
14	52.6	261	12	US-10-007-805-206	Sequence 206, App
15	52.6	262	12	US-10-033-528-1836	Sequence 1836, Ap
16	52.6	267	10	US-09-294-0938-1896	Sequence 1896, Ap
17	52.6	268	10	US-09-923-876-5857	Sequence 5857, Ap
18	52.6	271	10	US-09-783-590-11139	Sequence 11139, A
19	52.6	274	10	US-09-867-701-5278	Sequence 5278, Ap

20	52.6	280	10	US-09-878-574-246	Sequence 246, App
21	52.6	283	10	US-09-294-0938-3259	Sequence 3259, Ap
22	52.6	293	10	US-09-294-0938-6179	Sequence 6179, Ap
23	52.6	306	10	US-09-974-300-8100	Sequence 8100, Ap
24	52.6	339	10	US-09-878-574-1186	Sequence 1186, Ap
25	52.6	351	9	US-09-938-842A-1451	Sequence 1451, Ap
26	52.6	358	9	US-09-728-444-594	Sequence 594, App
27	52.6	363	10	US-09-770-791-478	Sequence 478, App
28	52.6	365	10	US-09-653-817-177	Sequence 177, App
29	52.6	367	10	US-09-878-574-2907	Sequence 2907, Ap
30	52.6	373	10	US-09-867-701-6841	Sequence 6841, Ap
31	52.6	381	10	US-09-878-574-2423	Sequence 2423, Ap
32	52.6	383	10	US-09-878-574-1113	Sequence 1113, Ap
33	52.6	389	10	US-09-960-352-5604	Sequence 5604, Ap
34	52.6	392	10	US-09-884-441-372	Sequence 372, App
35	52.6	396	10	US-09-970-300A-1484	Sequence 1484, Ap
36	52.6	396	12	US-10-033-528-1484	Sequence 1484, Ap
37	52.6	399	10	US-09-878-574-4036	Sequence 4036, Ap
38	52.6	402	10	US-09-878-574-3909	Sequence 3909, Ap
39	52.6	405	10	US-09-969-708-35	Sequence 35, App1
40	52.6	405	10	US-09-974-300-8367	Sequence 8367, Ap
41	52.6	411	9	US-09-938-842A-4215	Sequence 4215, Ap
42	52.6	418	10	US-09-919-580-485	Sequence 485, App
43	52.6	419	10	US-09-983-965-2492	Sequence 2492, App
44	52.6	437	10	US-09-920-300A-500	Sequence 500, App
45	52.6	437	12	US-10-033-528-500	Sequence 500, App
46	52.6	439	10	US-09-770-444-941	Sequence 941, App
47	52.6	440	10	US-09-895-828-293	Sequence 293, App
48	52.6	442	10	US-09-960-352-4337	Sequence 437, App
49	52.6	445	10	US-09-878-574-4615	Sequence 4615, Ap
50	52.6	458	10	US-09-925-300-794	Sequence 794, App
51	52.6	460	10	US-09-864-761-22182	Sequence 22182, A
52	52.6	463	10	US-09-878-574-4545	Sequence 4545, Ap
53	52.6	476	10	US-09-864-761-14174	Sequence 14174, A
54	52.6	476	10	US-09-783-590-11499	Sequence 11499, A
55	52.6	480	10	US-09-864-761-11304	Sequence 11304, A
56	52.6	488	10	US-09-783-590-84	Sequence 84, App1
57	52.6	510	10	US-09-920-300A-1592	Sequence 1592, Ap
58	52.6	510	12	US-10-033-528-1592	Sequence 1592, Ap
59	52.6	512	10	US-09-919-580-844	Sequence 844, App
60	52.6	512	10	US-09-783-590-9422	Sequence 9422, App
61	52.6	518	10	US-09-998-598-130	Sequence 33, App1
62	52.6	519	10	US-09-919-580-140	Sequence 140, App
63	52.6	529	10	US-09-998-598-2598	Sequence 2598, Ap
64	52.6	531	10	US-09-604-287A-123	Sequence 123, App
65	52.6	531	10	US-09-339-338-123	Sequence 123, App
66	52.6	533	12	US-10-007-805-123	Sequence 123, App
67	52.6	533	10	US-09-919-580-351	Sequence 351, App
68	52.6	534	10	US-09-919-580-483	Sequence 483, App
69	52.6	534	10	US-09-920-300A-633	Sequence 633, App
70	52.6	534	12	US-10-033-528-633	Sequence 633, App
71	52.6	536	10	US-09-919-580-593	Sequence 593, App
72	52.6	537	10	US-09-919-580-236	Sequence 236, App
73	52.6	537	10	US-09-919-580-518	Sequence 518, App
74	52.6	541	10	US-09-919-580-502	Sequence 502, App
75	52.6	550	10	US-09-813-358-191	Sequence 191, App
76	52.6	553	10	US-09-833-381-1568	Sequence 1568, Ap
77	52.6	555	10	US-09-924-033A-140	Sequence 140, App
78	52.6	556	10	US-09-919-580-316	Sequence 316, App
79	52.6	561	10	US-09-919-580-556	Sequence 556, App
80	52.6	563	10	US-09-917-800A-825	Sequence 825, App
81	52.6	564	10	US-09-919-580-310	Sequence 310, App
82	52.6	564	10	US-09-919-580-535	Sequence 533, App
83	52.6	567	10	US-09-919-580-335	Sequence 339, App
84	52.6	570	10	US-09-919-580-468	Sequence 468, App
85	52.6	573	10	US-09-919-580-360	Sequence 360, App
86	52.6	579	10	US-09-919-580-227	Sequence 227, App
87	52.6	589	10	US-09-919-580-560	Sequence 560, App
88	52.6	595	10	US-09-864-761-8882	Sequence 8882, Ap
89	52.6	595	10	US-09-814-292-45	Sequence 45, App1
90	52.6	599	10	US-09-864-761-8472	Sequence 8472, Ap

ALIGNMENTS

RESULT 1

US-09-402-100-35/c
; Sequence 35, Application US/09402100
; Patent No. US20010019834A1
; GENERAL INFORMATION:
; APPLICANT: Daewoong Pharmaceutical Co, LTD
; APPLICANT: Kim, Byung-O
; APPLICANT: Shin, Sung-Seup
; APPLICANT: Yu, Young-Hyo
; APPLICANT: Park, Myung-Hwan
; APPLICANT: Choi, Deok-Joon
; APPLICANT: Jung, Hyun-Jin
; TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helicobacter pylori
; FILE REFERENCE: 0136/OG140
; CURRENT FILING DATE: 1999-09-27
; EARLIER FILING DATE: 1997-03-31
; EARLIER APPLICATION NUMBER: KR 97-11950
; EARLIER FILING DATE: 1997-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Oligonucleotide
US-09-402-100-35

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 25;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 20 CCAATTTTTCACATCCACG 2

RESULT 2

US-09-969-373-1152/c
; Sequence 1152, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1152
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1152

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 100;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 97 CCAATCATTTCCATCCACG 79

RESULT 3

US-09-867-701-3962
; Sequence 3962, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3962
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3962

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 123;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 4 CCAATCTGTCGACACG 22

RESULT 4

US-09-974-300-8096/c
; Sequence 8096, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8096
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8096

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 210;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 152 CCAATTTGCTGTCCACG 134

RESULT 5

US-09-778-320-59/c

```

Sequence 59, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(214)
OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59

```

```

Query Match      52.6%; Score 10; DB 10; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAGC 19
    |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 6
US-09-910-689-59/C
Sequence 59, Application US/09910689
Patent No. US20020081609A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C6
CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197
OTHER INFORMATION: n = A,T,C or G
US-09-910-689-59

```

```

Query Match      52.6%; Score 10; DB 10; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAGC 19
    |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 7
US-10-010-742-59/C
Sequence 59, Application US/10010742
Patent No. US20020146727A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C7
CURRENT APPLICATION NUMBER: US/10/010,742
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197
OTHER INFORMATION: n = A,T,C or G
US-10-010-742-59

```

```

Query Match      52.6%; Score 10; DB 12; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAGC 19
    |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 8
US-09-783-590-10136
Sequence 10136, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16 2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10136
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or c

```

```
NAME/KEY: misc feature
LOCATION: (17)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (48)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (134)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (145)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (150)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (182)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (186)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (187)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (205)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10136
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 219;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAGC 19
Db 99 CCAATTACACACCCAGC 117
```

```
RESULT 9
US-09-777-564-1013
Sequence 1013, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: Mammion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 1013
LENGTH: 237
TYPE: DNA
ORGANISM: Homo sapiens
US-09-777-564-1013
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 237;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCAGC 19
Db 18 CCAATTACACCCAGC 36
```

```
RESULT 10
US-09-960-352-13155/C
Sequence 13155, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Ningbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 1511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13155
LENGTH: 238
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-LIB34-004-Q1-E1-F8
US-09-960-352-13155
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 238;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAGC 19
Db 159 CCAATTATGTTAGATCCAGC 141
```

```
RESULT 11
US-09-878-574-6181/C
Sequence 6181, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR APPLICATION NUMBER: 2001-12-21
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 6181
LENGTH: 247
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701097950H1
US-09-878-574-6181
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 247;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAGC 19
Db 242 CCAATTAAGTGTCCAGC 224
```

```
RESULT 12
US-09-604-287A-206
Sequence 206, Application US/09604287A
Patent No. US20020064872A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yudi
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
```



```

; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-206

Query Match          52.6%; Score 10; DB 10; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAG 19
    |||||
DB 140 CCAATCTTCATCTCCAG 158

```

```

RESULT 13
US-09-339-338-206
; Sequence 206, Application US/09339338A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-206

Query Match          52.6%; Score 10; DB 10; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAG 19
    |||||
DB 140 CCAATCTTCATCTCCAG 158

```

```

RESULT 14
US-10-007-805-206
; Sequence 206, Application US/10007805
; Patent No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10

```

```

; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-206

Query Match          52.6%; Score 10; DB 12; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAG 19
    |||||
DB 140 CCAATCTTCATCTCCAG 158

```

```

RESULT 15
US-10-033-528-1836
; Sequence 1836, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1836
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1836

Query Match          52.6%; Score 10; DB 12; Length 262;
Best Local Similarity 52.6%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAG 19
    |||||
DB 144 CCAATCTTCATCTCCAG 162

```

```

RESULT 16
US-09-294-093B-1896
; Sequence 1896, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 1896
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700345158H1

```

```

; NAME/KEY: unsure
; LOCATION: 8, 24, 45, 69, 106, 174, 192, 197, 199-200, 206-207, 209, 227, 257, 260
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-1896

```

```

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 267;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCACG 19
DB 214 CCAATCGCGCGAGGCCACG 232

```

```

RESULT 17
; Sequence 5857, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Itc)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIORITY FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5857
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700457860H1
; LOCATION: 65, 202, 216
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5857

```

```

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 268;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCACG 19
DB 9 CCAATCGCGCGAGGCCACG 27

```

```

RESULT 18
; Sequence 1139, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIORITY FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 11139
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (56)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (92)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (216)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (251)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (253)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (258)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (259)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (266)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11139

```

```

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 271;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCACG 19
DB 102 CCAATCGAGTMAACACG 84

```

```

RESULT 19
; Sequence 5278, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilante, Paul A.
; APPLICANT: Jones, Robert
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; PRIORITY FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5278
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-5278

```

```

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 274;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 150 CCAATTAACAGGCCACG 132

RESULT 20

US-09-878-574-246
; Sequence 246, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 246
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-D5
US-09-878-574-246

Query Match 52.6%; Score 10; DB 10; Length 280;
Best Local Similarity 52.6%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 135 CCAATCATCATGCACG 153

RESULT 21

US-09-294-093B-3259
; Sequence 3259, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3259
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 70037672H1
; LOCATION: 33, 53
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3259

Query Match 52.6%; Score 10; DB 10; Length 283;
Best Local Similarity 52.6%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 4 CCAATCCCTTCCACG 22

RESULT 22

US-09-294-093B-6179
; Sequence 6179, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 6179
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700383150H1
; LOCATION: 280, 255-256
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-6179

Query Match 52.6%; Score 10; DB 10; Length 293;
Best Local Similarity 52.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 54 CCAATATCTATTGCCACG 72

RESULT 23

US-09-974-300-8100
; Sequence 8100, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8100
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(306)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8100

Query Match 52.6%; Score 10; DB 10; Length 306;
Best Local Similarity 52.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||

Db 94 CCAATTCGCTGTCCACG 112

RESULT 24

US-09-878-574-1186/C
; Sequence 1186, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1186
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-041-Q1-B1-A12
US-09-878-574-1186

Query Match 52.6%; Score 10; DB 9; Length 339;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 164 CCAATGAATGTAACACG 146

RESULT 25

US-09-938-842A-1451/C
; Sequence 1451, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: S1300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1451
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1451

Query Match 52.6%; Score 10; DB 9; Length 351;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 143 CCAATCAGAGCTGCCACG 125

RESULT 26
US-09-728-444-594/C

; Sequence 594, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0100-USA
; CURRENT APPLICATION NUMBER: US/09/728, 444
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168, 360
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(358)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-594

Query Match 52.6%; Score 10; DB 9; Length 358;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 95 CCAATCTCCAAGGCCACG 77

RESULT 27

US-09-770-791-478
; Sequence 478, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kitzker, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Horban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770, 791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178, 480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-478

Query Match 52.6%; Score 10; DB 10; Length 363;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 105 CCAATCAGCTCAGCCACG 123

RESULT 28
US-09-563-817-177
; Sequence 177, Application US/09563817
; Patent No. US20020095031A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020095031A1e1 Human Polynucleotides and the
; FILE REFERENCE: LEX-0021-USA
; CURRENT APPLICATION NUMBER: US/09/563,817
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/132,343
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 365
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(365)
; OTHER INFORMATION: n = A,T,C or G
US-09-563-817-177

Query Match 52.6%; Score 10; DB 10; Length 365;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 244 CCAATTCCTCATCCACG 262

RESULT 29
US-09-878-574-2907
; Sequence 2907, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 2907
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-018-Q1-H1-D9
US-09-878-574-2907

Query Match 52.6%; Score 10; DB 10; Length 367;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 197 CCAATCAGCTGAGCCACG 215
|||||

RESULT 30
US-09-867-701-6841/c
; Sequence 6841, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aqlate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6841
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-6841

Query Match 52.6%; Score 10; DB 10; Length 373;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 202 CCAATATAGTAAACCACG 184

Search completed: November 16, 2002, 04:29:24
Job time : 49 secs

